

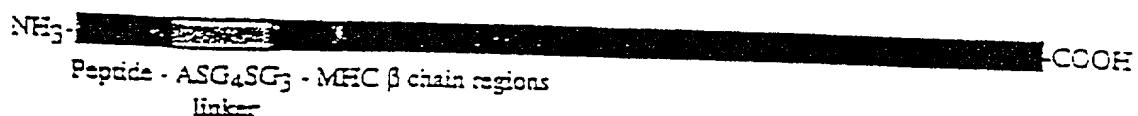
Figure 1A. Peptide-linker- β chain construct

Figure 1B. Schematic view of peptide-linked MHC binding groove

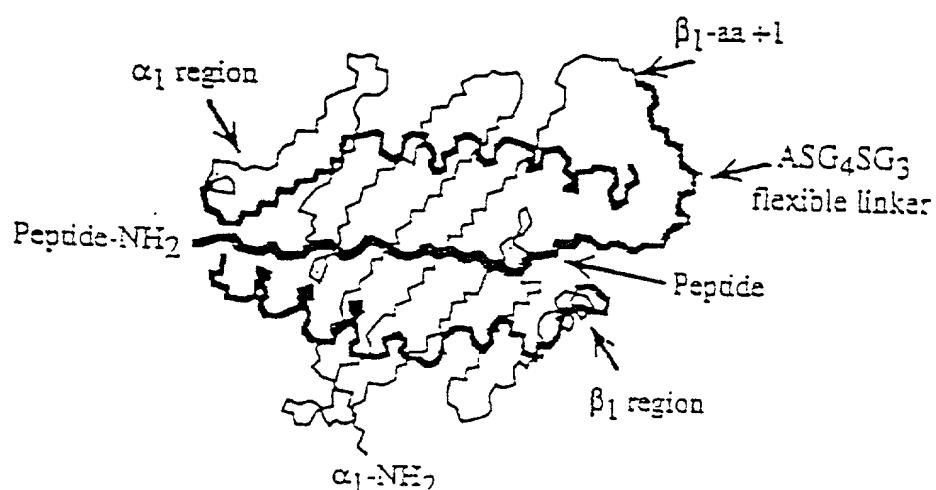
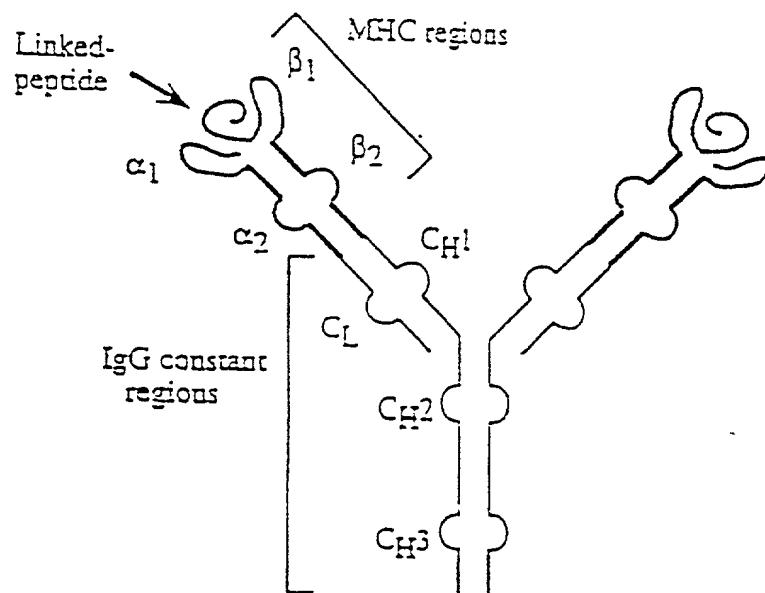
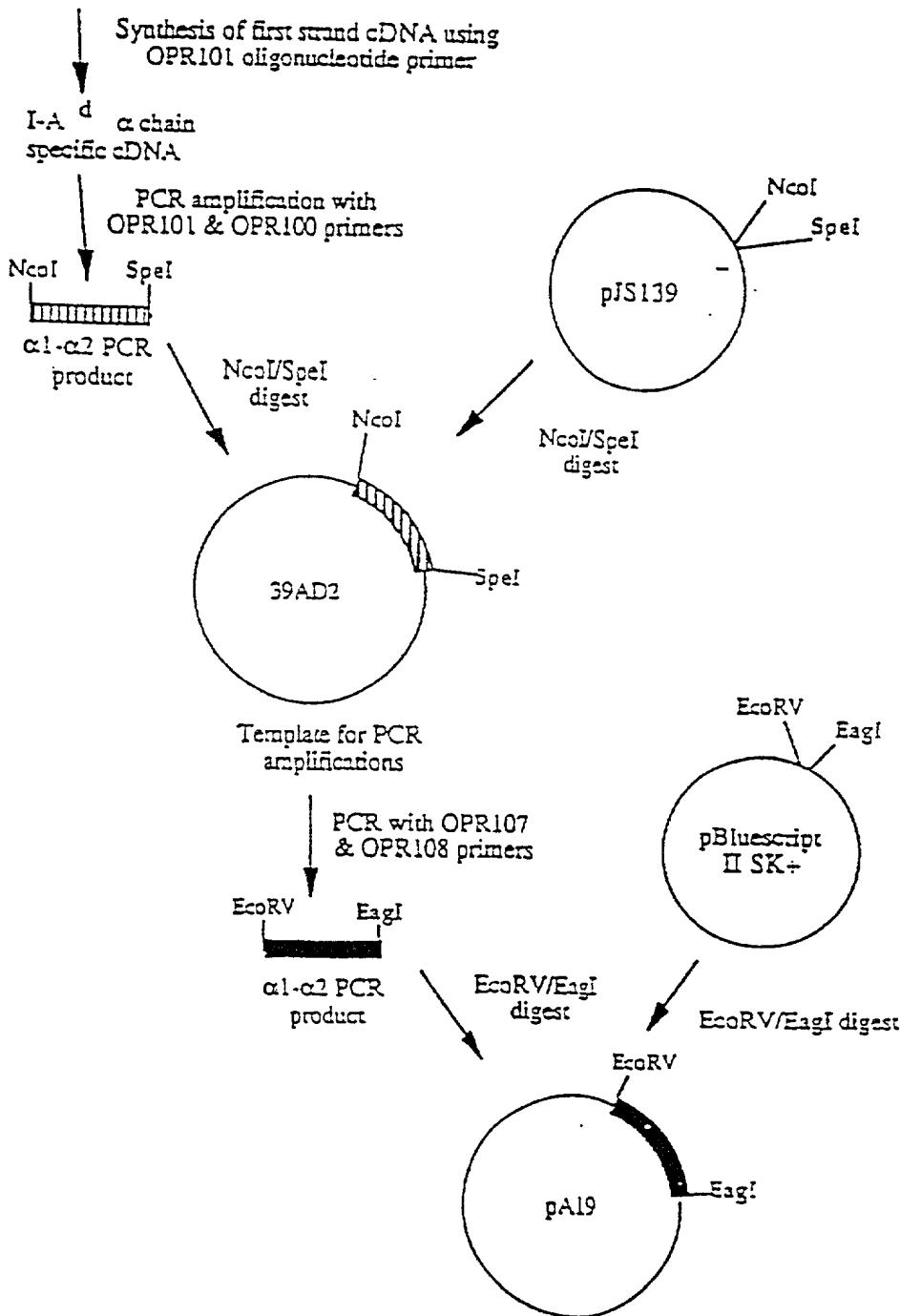


Figure 1C. Schematic view of soluble peptide-linked MHC-IgG C-region fusion protein



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Figure 2: I-A^d α chain cloning schemeTotal RNA isolated
from A20 cells

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Figure 3: I-A^d β chain cloning scheme

Total RNA isolated
from A20 cells

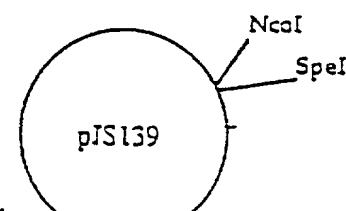
↓
Synthesis of first strand cDNA using
oligo dT primer

cDNA template

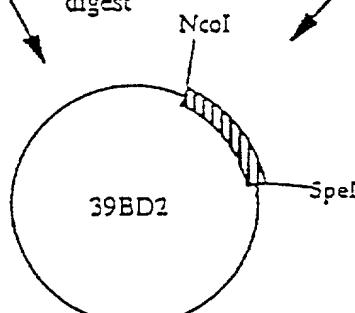
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PCR amplification with
OPR102 & OPR104 primers

NcoI SpeI

 β 1- β 2 PCR
product



NcoI/SpeI
digest

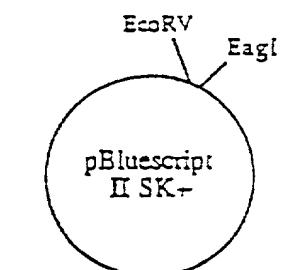


Template for PCR
amplifications

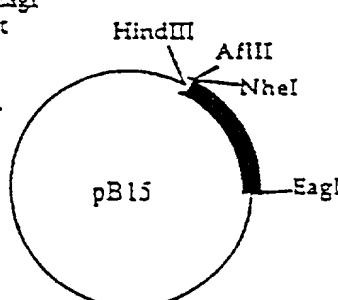
↓
PCR with OPR106
& OPR112 primers

EcoRV EagI

NheI
AflII
Linker- β 1- β 2
PCR product



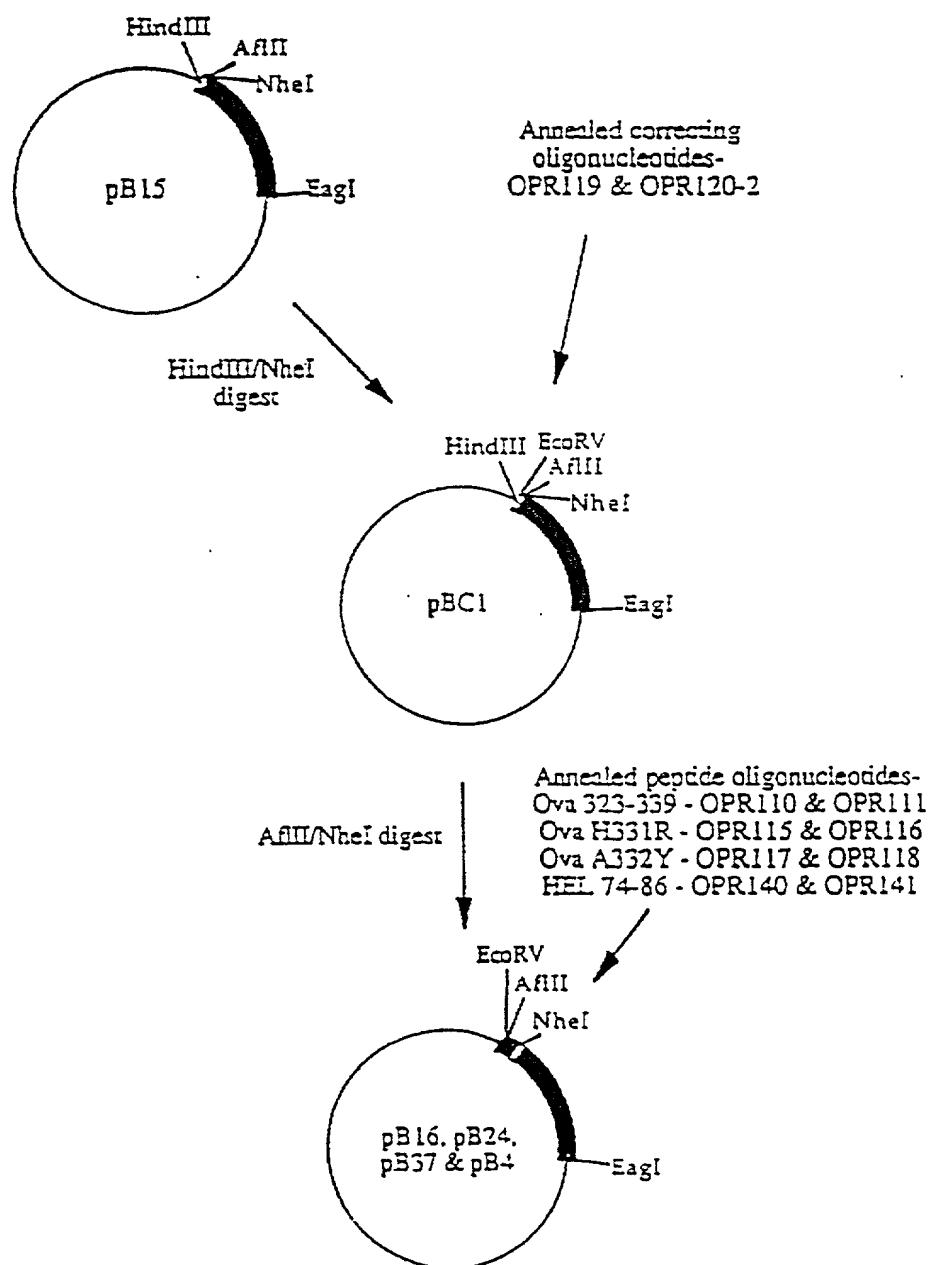
EcoRV/EagI digest



Mutation in linker region-
no EcoRV site present

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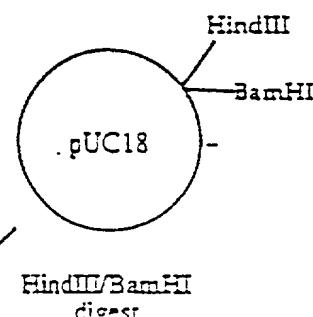
Figure 3: cont.



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Figure 4: HLA-DR1 α chain cloning schemeTotal RNA isolated
from BLCL K68 cellsSynthesis of first strand cDNA using
oligo-dT primercDNA
templatePCR amplification with
DRI1A-B & DRI1A-F primers

HindIII BamHI

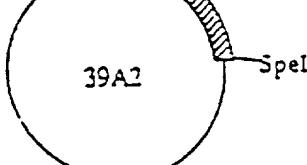
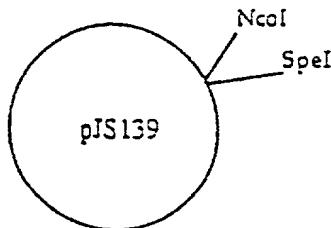
 α 1- α 2-hinge
PCR productHindIII/BamHI
digestHindIII
digestHindIII/BamHI
digestTemplate for PCR
amplificationsPCR with AF-N &
AB-S primers

NcoI SpeI

 α 1- α 2-hinge
PCR product

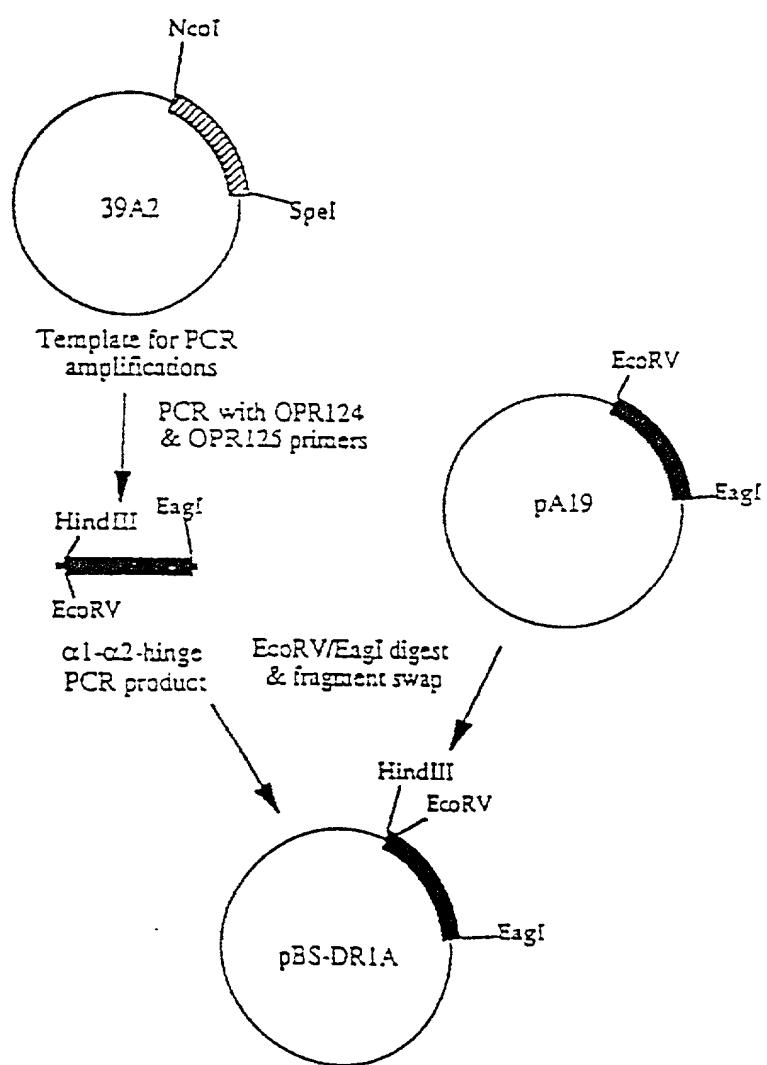
NcoI/SpeI digest

NcoI

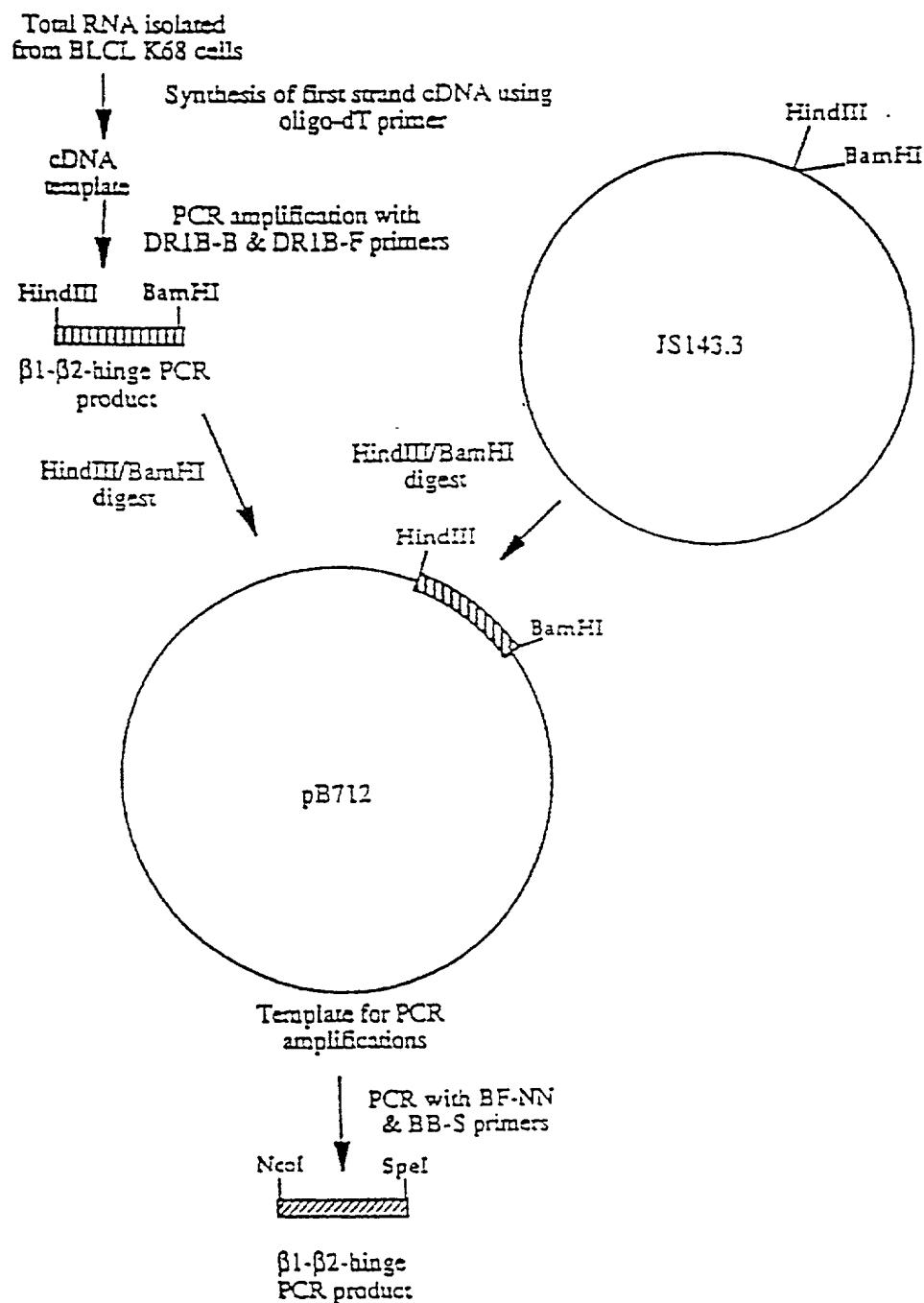
Template for PCR
amplifications

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Figure 4: cont.

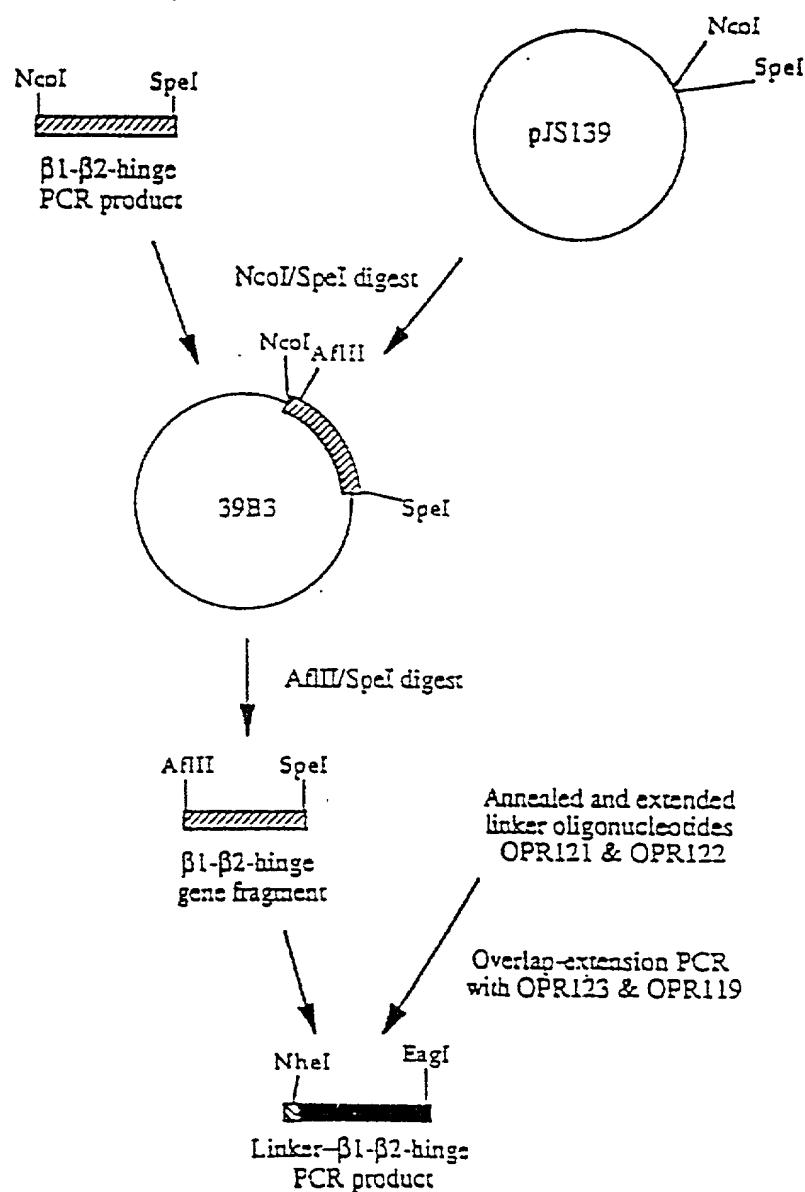


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Figure 5: HLA-DR1 β chain cloning scheme

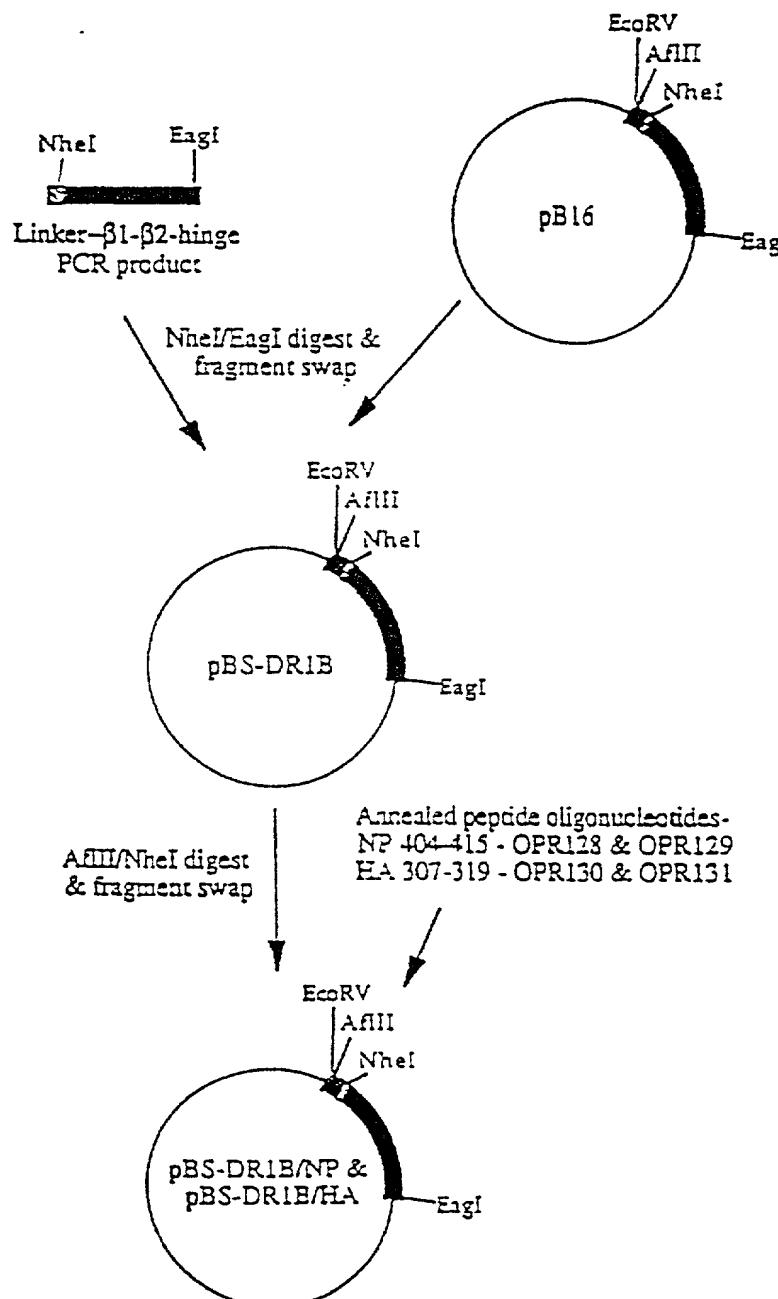
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Figure 5: cont.



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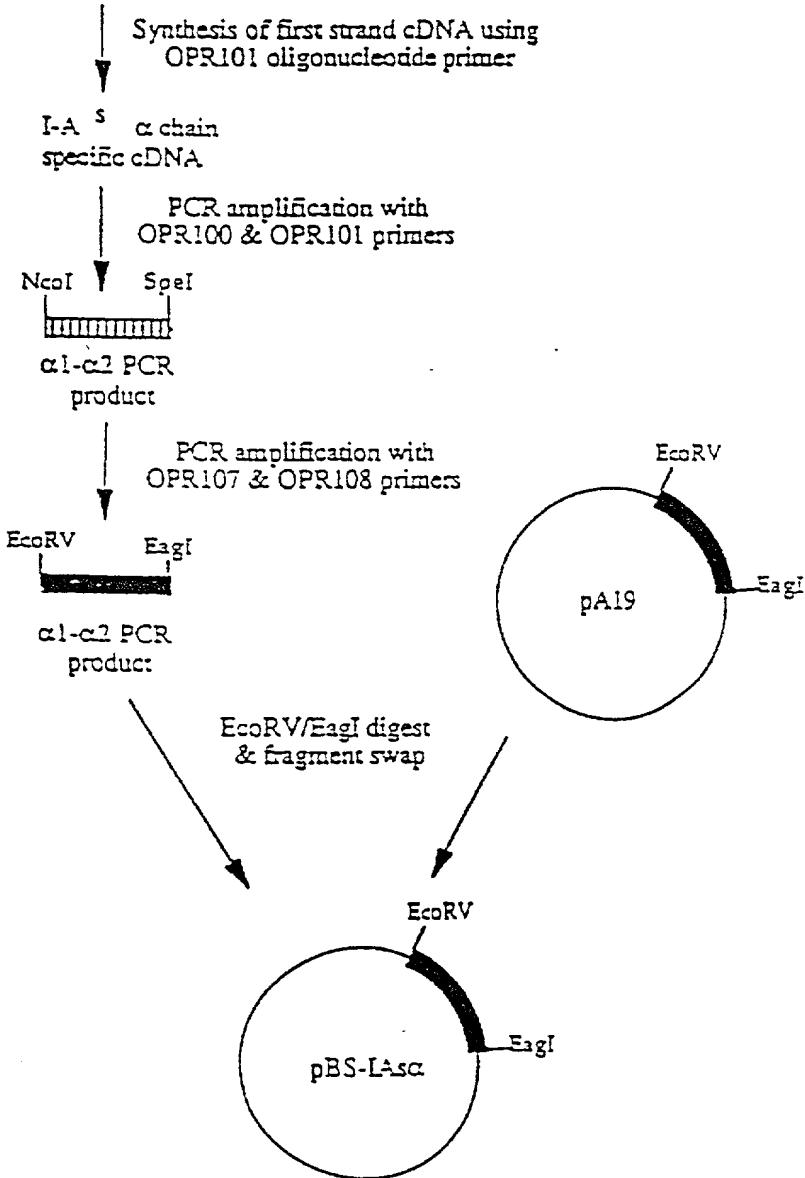
Figure 5: cont.



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Figure 6: I-A^S α chain cloning scheme

Total RNA isolated from
SJL mouse spleen cells



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Figure 7: I-A^s β chain cloning scheme

Total RNA isolated from
SJL mouse spleen cells

↓
Synthesis of first strand cDNA using
OPR106 primer

I-A^s β specific
cDNA template

↓
PCR amplification with
VW310 & OPR106 primers

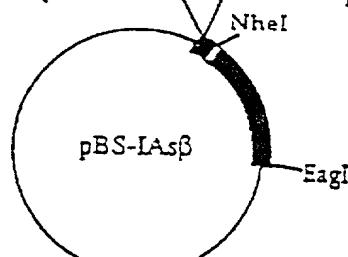
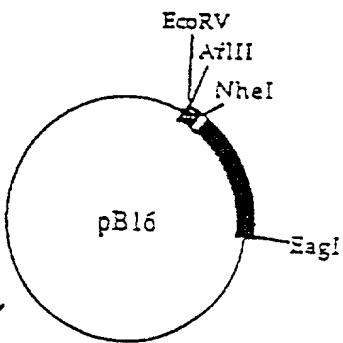
β1-β2 PCR product

↓
PCR amplification with
VW309 & OPR106 primers

NheI EagI

Linker-β1-β2
PCR product

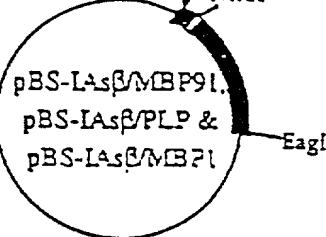
NheI/EagI digest &
fragment swap



NheI/EagI
digest

Annealed peptide oligonucleotides-
MBP 91-103 - VW315 & VW316
PLP 139-151 - VW313 & VW314
MBP 1-14 - VW317 & VW318

AfIII/NheI digest
& fragment swap



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Figure 8 - Oligonucleotides used in constructing MHC vectors

I-A^d/I-A^s PCR primers and cloning oligonucleotides (restriction site are underlined).

OPR100

5'-GGG GGG GCC ATG GCC GAA GAC GAC ATT GAG GCC GAC-3'

OPR101

5'-GGG GGG ACT AGT CCA GTG TTT CAG AAC CGG CTC-3'

OPR107

5'-CCC CCC GAT ATC TCA GCT TCC AGC AGT GGA GAC GAC ATT GAG
GCC G-3'

OPR108

5'-CCC CCC CGG CCG TCA CTT AGG TCC CCA GTG TTT CAG AAC CGG
C-3'

OPR102

5'-GGG GGG ATG GGC GGA AAC TCC GAA AGG CAA CTC G-3'

OPR104

5'-GGG GGG ACT AGT CCA CTC CRC AGT GAT GGG GC-3'

OPR106

5'-CCC CCC CGG CCG TAC CTG AGG ACC ACT CCA CAG TCA TGG-3'

OPR112

5'-CCC CCC GAT ATC ACA GGT GTC TTA AGT GCT AGC GCA GGG GGC
GCA AGC GGC GGA GGG GGA AAC TCC GAA AGG CAA TTC TTC-3'

OPR119

5'-AGC TTG ACA TCA CAG GTG TCT TAA GTG GAG-3'

OPR120-2

5'-CTA GCT CCA CTT AAG ACA CCT GTG ATA TCA-3'

VW310

5'-TCC GCA GGC GGC GGA GAC TCC GAA AGG CAA TTC G-3'

VW309

5'-CGA TCG CTA CGG CGG GTG GTG GTT CGG GTG GCG CGG GAG-3'

OPR136

5'-CCC CCC AGG CTT CCC GGG CCA CCA TCC CGT GCA GCA GAG CTC
TG-3'

OPR139

5'-CCC CCC GAG CTC GAA TTC TCA TAA AGG CCC TGG GTG TCT G-3'

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Figure 8 - cont

OPR132

5'-CCC CCC AAG CTT CCC GGG CCA CCA TGG CTC TGC AGA TCC CCA
GC-3'

OPR133

5'-CCC CCC ACT TTA GGT CCT TGG GCT GGT CAG CAC C-3'

OPR134

5'-CCC CCC CCA TCA CTG TGG AGT GGA GGG-3'

OPR135

5'-CCC CCC GAG CTC GAA TTC TCA CTG CAG GAG CCC TGC TGG-3'

HLA-DRI PCR primers and cloning oligonucleotides.

DR1A-F

5'-GGG GGG AAG CTT ATG ACC AAA GAA GAA CAT GTG ATC ATC-3'

DR1A-B

5'-GGG GGG GAA TCC GTT CTC TGT AGT CTC TGG GAG AGG-3'

DR1B-F

5'-GGG GGG AAG CTT ATG GGG GAC ACC CGA CCA CGT TTC TTG TGG
CAG C-3'

AF-N

5'-GGG GGG GCC ATG GCC ATC AAA GAA GAA CAT GTG ATC ATC-3'

AB-S

5'-GCG GCG ACT AGT GTT CTC TGT AGT CTC TGG GAG AGG-3'

OPR124

5'-GGG GGG AAG CTT GAT ATC TCA GCT TCC ACC AGT AGT ACC AAA
GAA GAA CAT GTG ATC-3'

OPR125

5'-GGG GGG CGG CCG CTA CTT ACG TTT CTC TGG GAG AGG GCT TGG
AGC-3'

DR1B-B

5'-GCG GCG GAA TCC CTT GCT CTG TGC AGA TTC AGA CC-3'

BF-NN

5'-GGG GGG GCC ATG GCC GCA TCC GCT AGC GGG GAC ACC CGA CCA
CGT TTC TTG-3'

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Figure 3 - cont.

BB-5

5'-GCC GCG ACT AGT CTT GCT CTG TGC AGA TTC AGA CCG-3'

OPR121

5'-GTT GTC TTA AGT GGA GCT AGC GCA GGG GGC GGG TCC GGA GGT
GGT GGG GAC ACC CG-3'

OPR122

5'-GAA ATG ACA TTC AAA CTT CAG CTG CCA CAA GAA ACG TGG TCG
GGT GTC CCC ACC ACC-3'

OPR123

5'-GGG GGG CGG CGG TAC CTG AGG ACT TGC TCT GTG CAG ATT CAG-
3'

Peptide oligonucleotides.

Ova 323-332

OPR110

5'-TTA AGT ATC TCT CAG GCT GTT CAC GCT GCT CAC GCT GAA ATC
AAC GAA GCT GGT CGT G-3'

OPR111

5'-CTA GCA CGA CCA GCT TCG TTG ATT TCA GCC TGA GCA GCG TGA
ACA GCC TGA GAG ATA C-3'

Ova H331R

OPR115

5'-TTA AGT ATC TCT CAG GCT GTT CAC GCT GCT CGG GCT GAA ATC
AAC GAA GCT GGT CGT G-3'

OPR116

5'-CTA GCA CGA CCA GCT TCG TTG ATT TCA GCC CGA GCA GCG TGA
ACA GCC TGA GAG ATA C-3'

Ova A332Y

OPR117

5'-TTA AGT ATC TCT CAG GCT GTT CAC GCT GCT CAC TAC GAA ATC
AAC GAA GCT GGT CGT G-3'

OPR118

5'-CTA GCA CGA CCA GCT TCG TTG ATT TCA TAC TCA GCA GCC TGA
ACA GCC TGA GAG ATA C-3'

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Figure 3 - cont.

HEL 74-86

OPRI140

5'-TTA AGT AAC CTG TGC AAC ATC CCC TGC AGC GCC CTG CTG AGC
TCC G-3'

OPRI141

5'-CTA GCG GAG CTC AGC AGG GCG CTG CAGAGGG ATG TTG CRC AGG
TTA C-3'

NP 404-415

OPRI129

5'-TTA AGT CAG ATC AGC GTG CAG CCC GCC TTC AGC GTG CAG G-3'

OPRI129

5'-CTA GCC TGC ACG CTG AAG GCG GGC TGA ACG CTG ATC TGA C-3'

HA 307-319

OPRI130

5'-TTA AGT CCC AAG TAC GTG AAG CAG AAC ACC CTG AAG CTG GCC
ACC G-3'

OPRI131

5'-CTA GCG GTG GCC AGC TTC AGG GTG TTC TGC TTC ACG TAC TTG
GGA C-3'

MBP 91-103

VW315

5'-TTA AGT CAC TAT GGC TCC CTG CCG CAG AAG TCC CAG CAC GGG
CGC G-3'

VW316

5'-CTA GCG CGC CCG TGC TGG GAC TTC TGC GGC AGG GAG CCA TAG
TGA C-3'

PLP 139-151

VW313

5'-TTA CTT CAC TCC CTG GGC AAG TGG CTG GGC CRC CCG GAC AAG
TTC G-3'

VW314

5'-CTA GCG AAC TTG TTC GGG TGG CCC AGC CAC TTG CCC AGG GAG
TGA C-3'

Figure 8 - cont.

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MBP 1-14

VW317

5'-TTA AGT ATG GCA TCC CAG AAG CGC CCG TCC CAG CGC TCC AAG
TAC CTG G-3'

VW316

5'-CTA GCC AGG TAC TTG GAG CGC TGG GAC GGG CGC TTC TGG GAT
GCC ATA C-3'

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Figure 9A. Soluble I-A^d α chain construct

EcoRV

10	20	30	40	550	560	570	580	XbaI										
GATATTCAGCT TCC ACC AGT GAA GAC GAC ATT GAG GCG GAC GAC // CGG GTT CTG AAA CAC TGG AAA CCT AAGTACGGGGCG																		
CTATAGCTTGA AGG TCC TCA CTT CTG CTG TAA CTC CGG CTG CTG // CGC CAA GAC TTT GTG ACC TTT GCA TTGATGGGGCG																		
S	S	S ₁	E	D	D	I	E	A	D	R	Y	V	L	K	H	W	K	R
aa192]																		

IgG κ chain Signal peptide I-A^d α chain IgG κ chain
intron cleavage site intron intron

Figure 9B.

Soluble I-A^d β chain construct

Restriction sites for insertion of
oligonucleotides encoding peptides of interest

EcoRV A413I NheI

10	20	30	40	50	60	70	XbaI											
GATATTCAGCT TCC ACC AGT GAA GCT AGC GGA GCG GCG GCA AGC GGC GCA GCG GCA AAC TCC GAA AGG CAT //																		
CTATAGCTTGA AGG ATT TCA CTT CGA TCC CCT CGG CGG CGG CGG CCT TCC AGG CCT TCC CGA //																		
V	L	S	G	A	S	G	G	G	S	G	G	G	G	N	S	E	R	H
+1																		

IgG κ chain Signal peptide Linker region I-A^d β chain
intron cleavage site intron intron

ATC ACT CTG GAG TGG TCC TCA GGT AGCTGGGGCG
TAG TGA CAC CCT ACC AGG AGT GCA TGGGGCG
I T V E W S S
aa189]

I-A^d β chain IgG κ chain
intron intron

Figure 9C.

Soluble I-A^s α chain construct

EcoRV

10	20	30	40	550	560	570	580	XbaI										
GATATTCAGCT TCC ACC AGT GAA GAC GAC ATT GAG GCG GAC GAC // CGG GTT CTG AAA CAC TGG AAA CCT AAGTACGGGGCG																		
CTATAGCTTGA AGG TCC TCA CTT CTG CTG TAA CTC CGG CTG CTG // CGC CAA GAC TTT GTG ACC TTT GCA TTGATGGGGCG																		
S	S	S ₁	E	D	D	I	E	A	D	R	Y	V	L	K	H	W	K	R
aa192]																		

IgG κ chain Signal peptide I-A^s α chain IgG κ chain
intron cleavage site intron intron

Figure 9 - cont.

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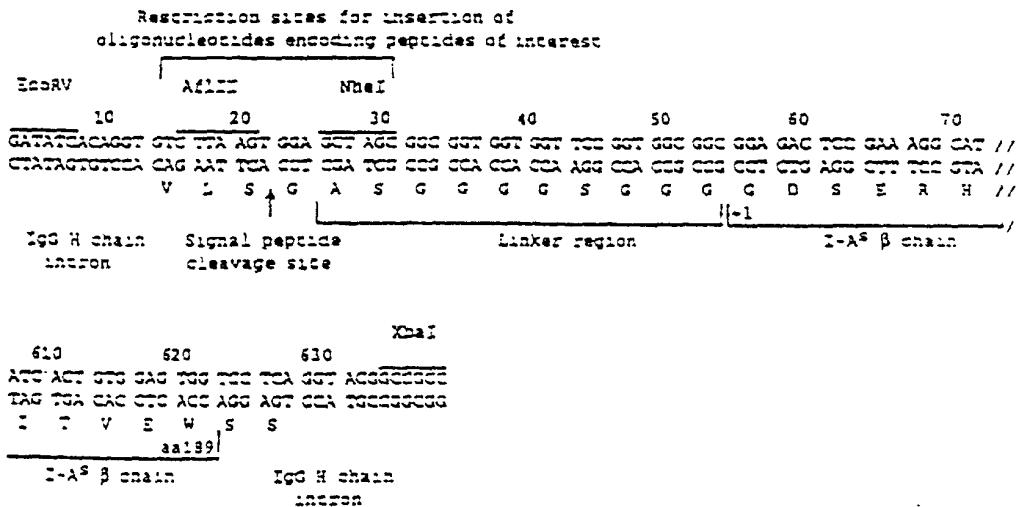
Figure 9D. Soluble I-A^S β chain construct

Figure 9E. Soluble HLA-DR1 α chain construct

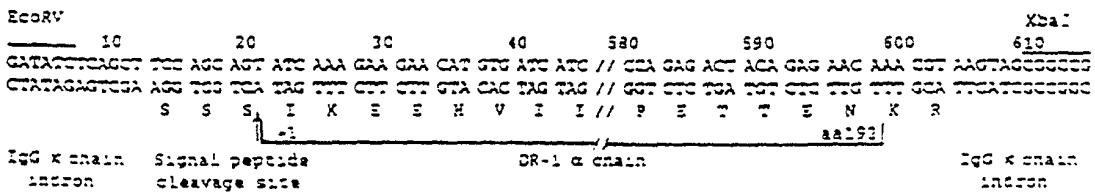
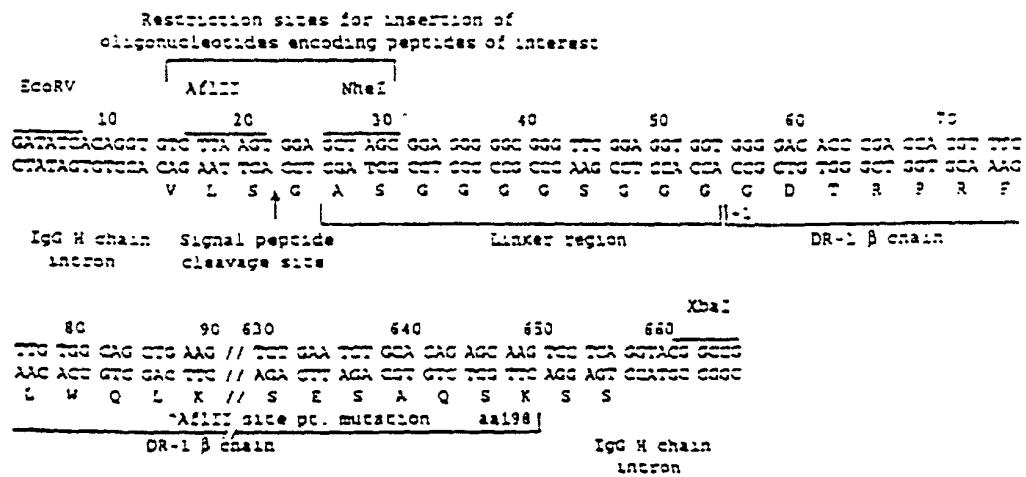


Figure 9F. Soluble HLA-DR1 β chain construct



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Figure 10. Original Mammalian Cell Expression Vectors

Figure 10A

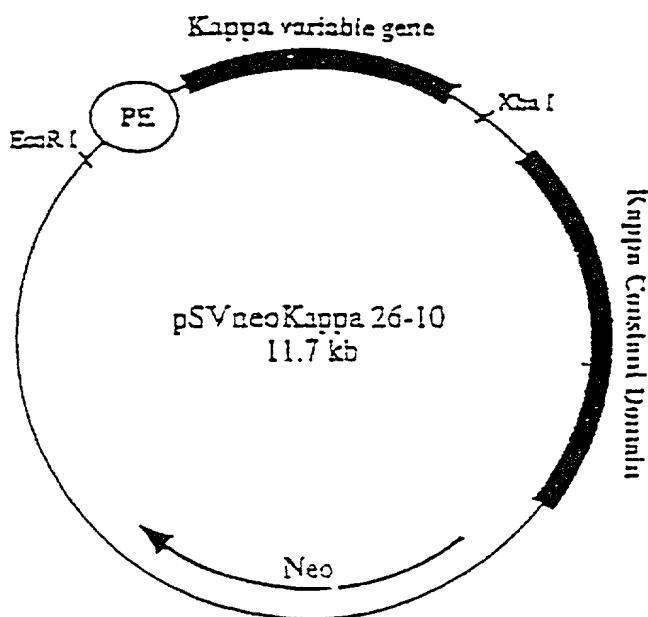
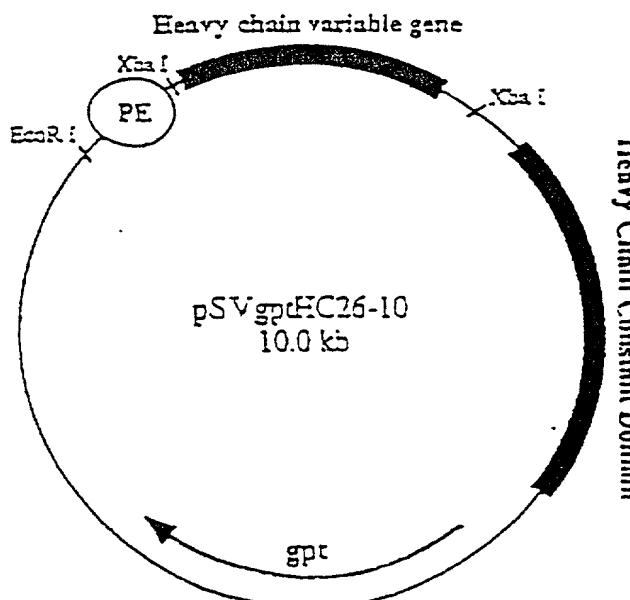


Figure 10B



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Figure 11. The 2.7 Kb Kappa and the 1.7 Kb Heavy Chain EcoR V and Eco I Mutated Constructs

Figure 11A

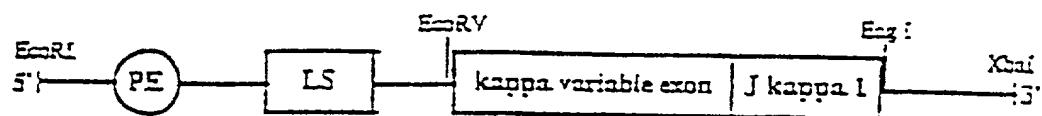
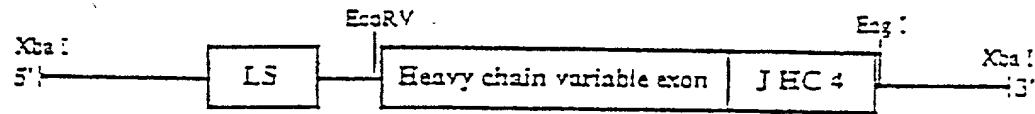
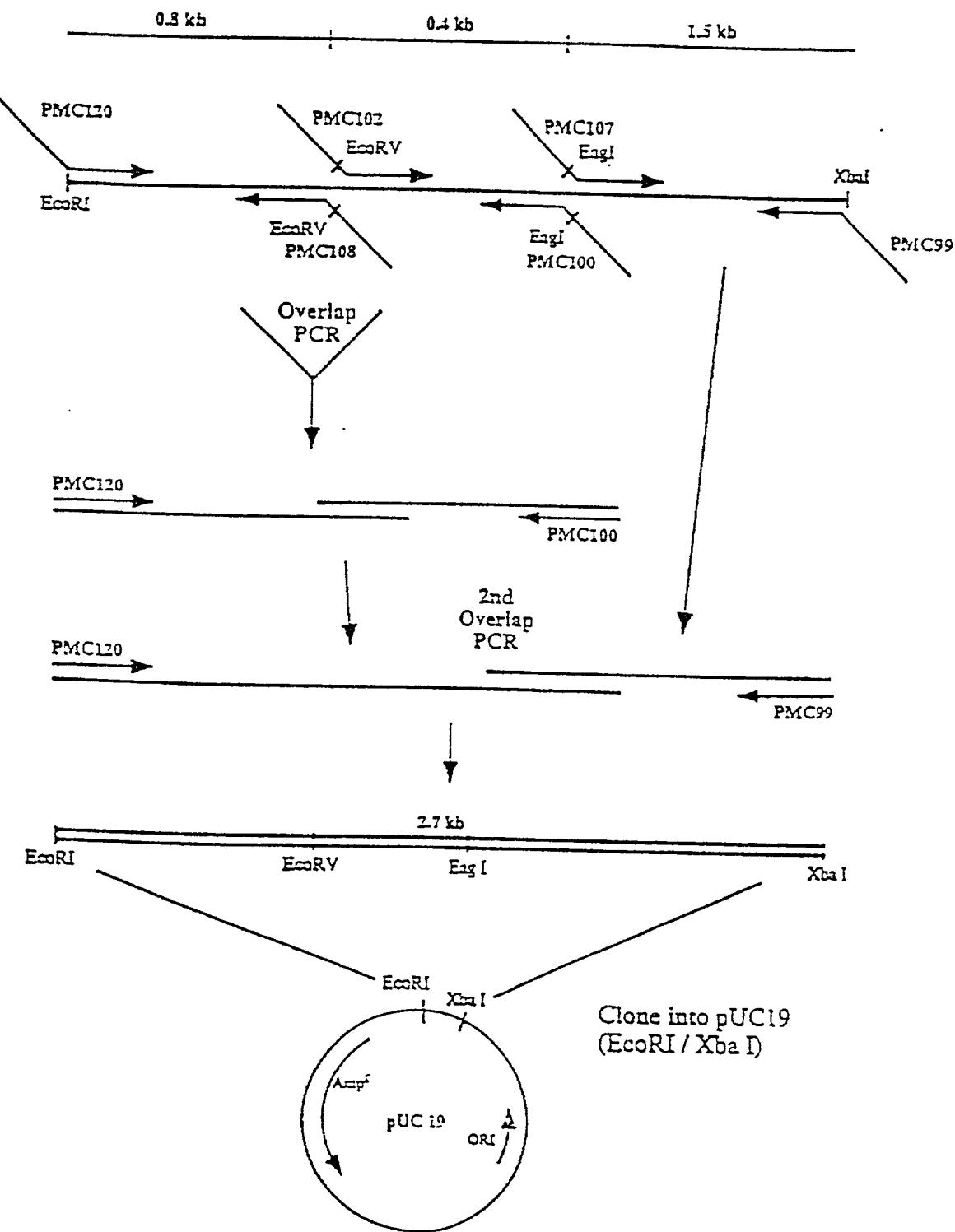


Figure 11B



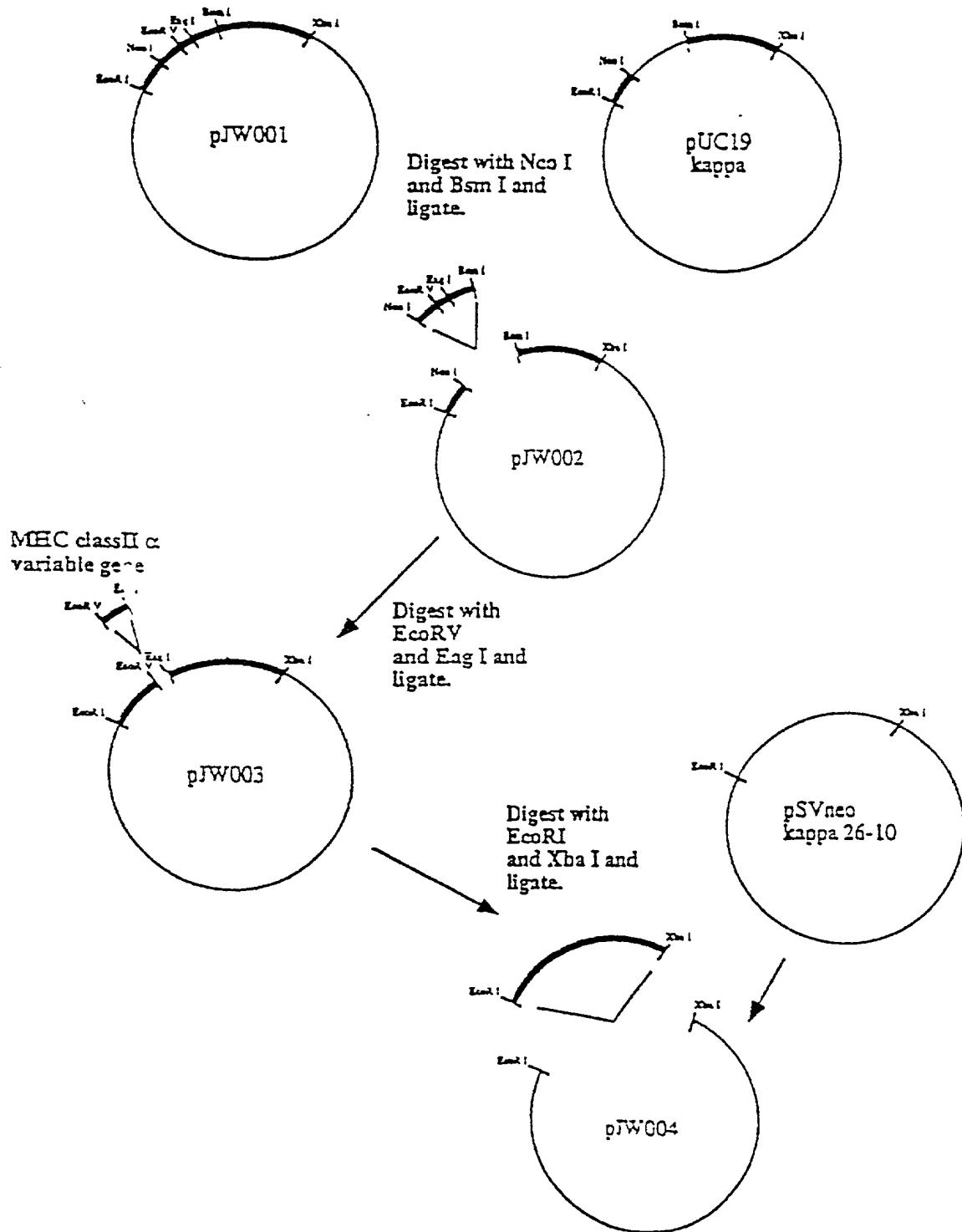
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Figure 12. PCR Site Directed Mutagenesis for Introducing EcoRV and EngI Restriction Sites into Kappa Chain 2.7kb Insert



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Figure 13. STRATEGY FOR CONSTRUCTING MHC CLASS II α / KAPPA CONSTANT GENE IN MAMMALIAN CELL EXPRESSION VECTOR

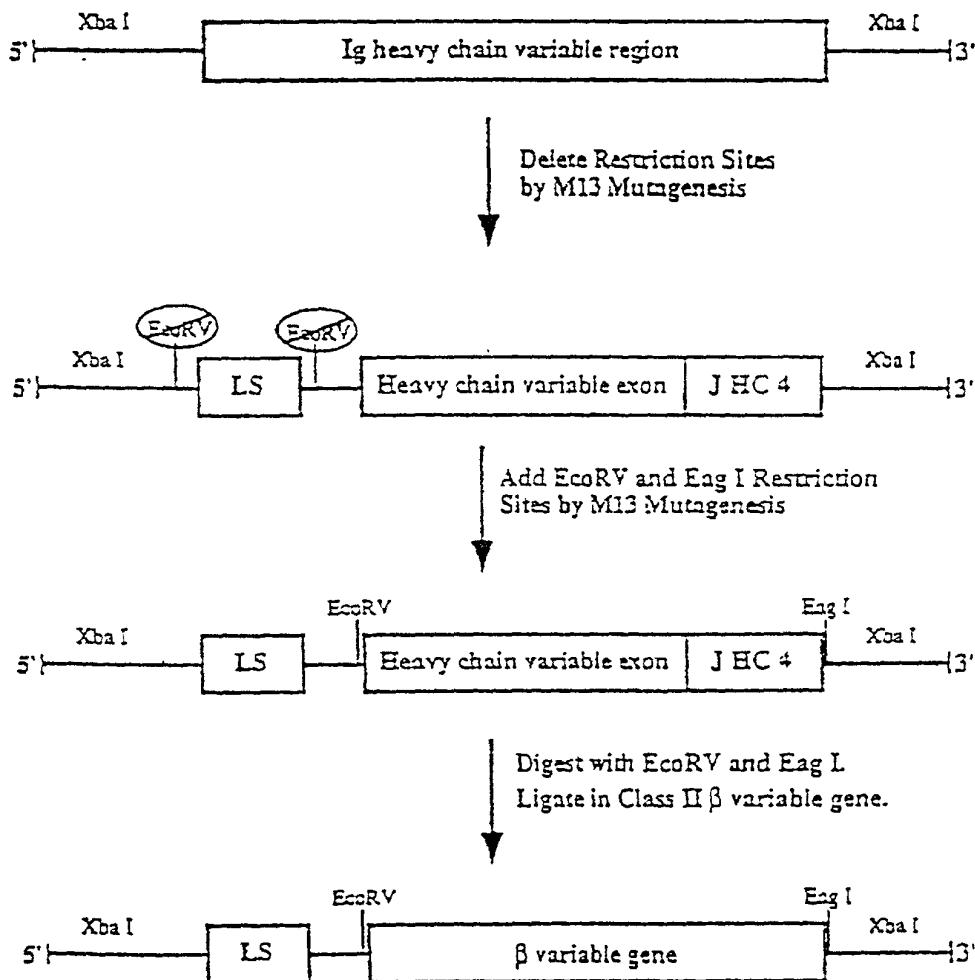


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Figure 14. Primers used for Sequencing Mutated 2.7 Kb Fragment

<u>Primer List</u>	<u>Sequence</u>
PMC-33	[5'GCTCAGCTGCTTGTTCAGTACTGATG']
PMC-77	[5'GTAAGTAGCGGCCG3']
PMC-111	[5'GGTATGTAAAAATAAACATCACAG3']
PMC-114	[5'GCTTGGCTACGGAGTTACTG']

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Figure 15. Strategy for M13 Mutagenesis and Cloning of the MEC II β Variable Gene

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Figure 16. Final Vectors for Expressing MEC II / Ig Chimeric Proteins

Figure 16A

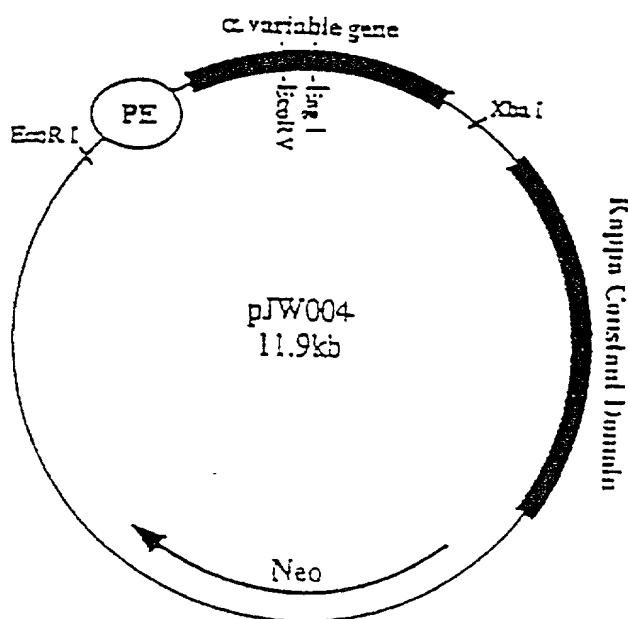
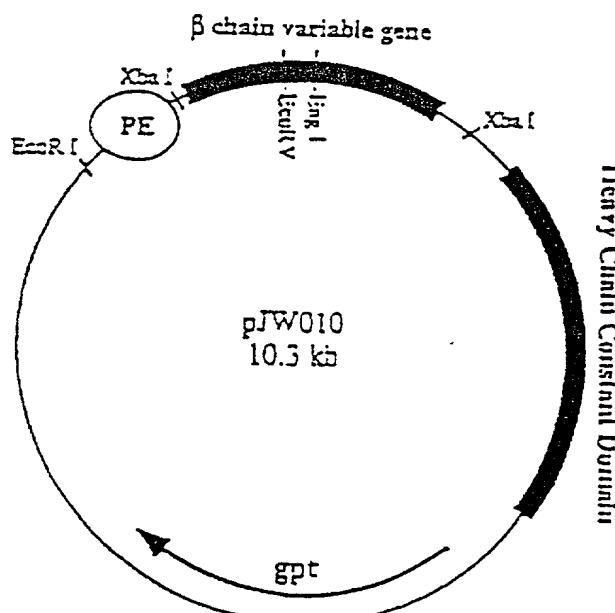
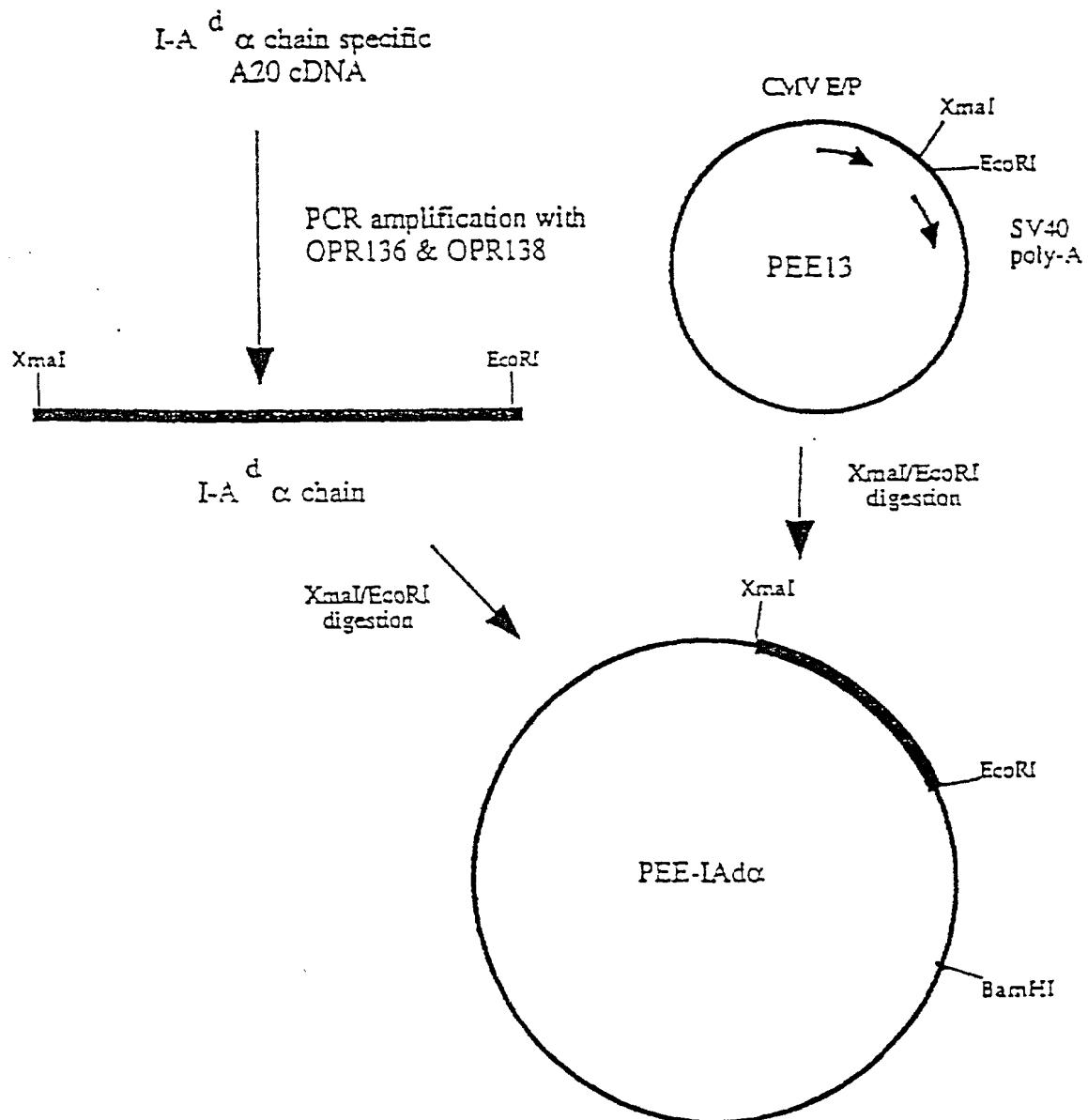


Figure 16B



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Figure 17 - Full length peptide linked MHC expression vectors



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Figure 17 - cont.

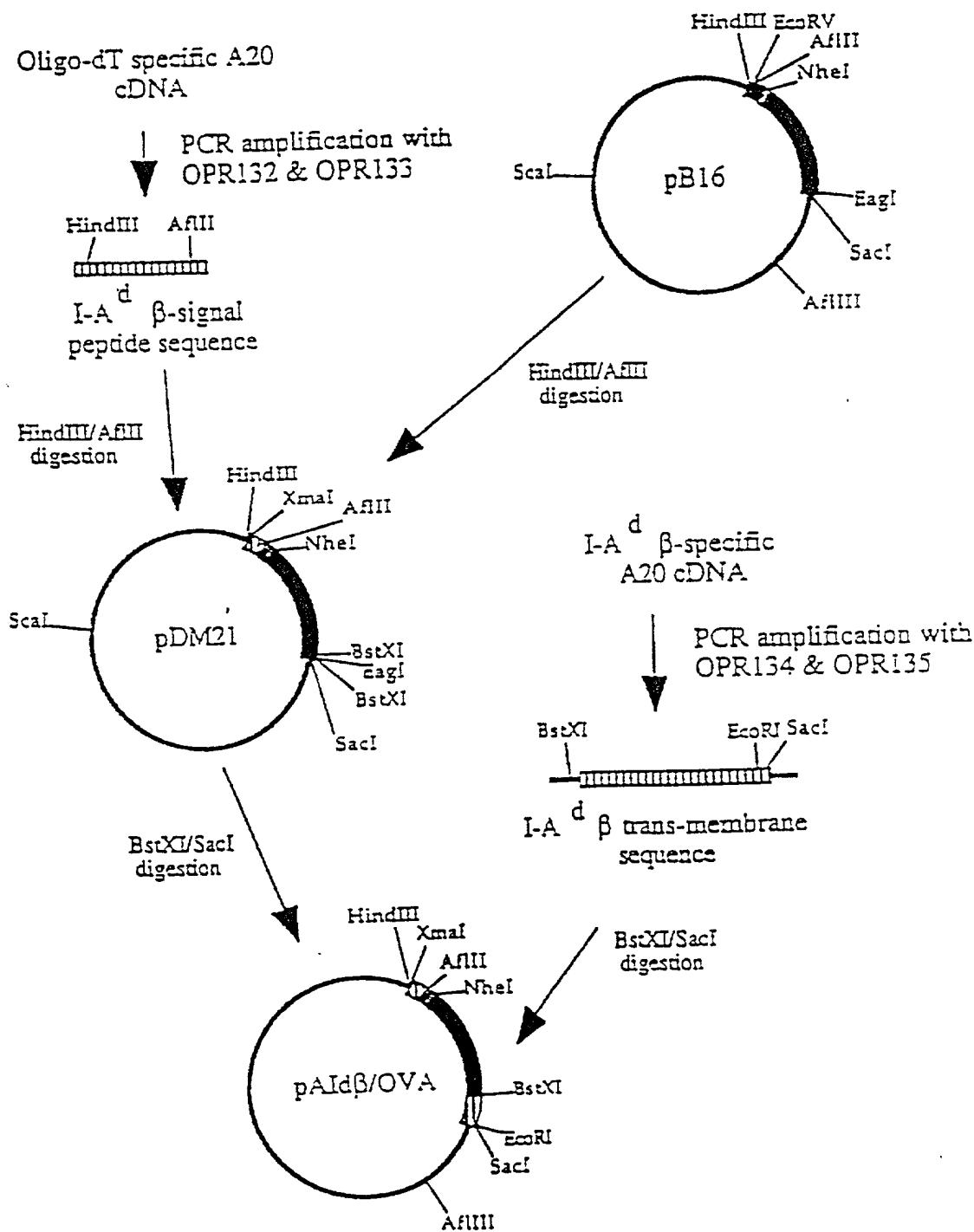


Figure 17 - cont.

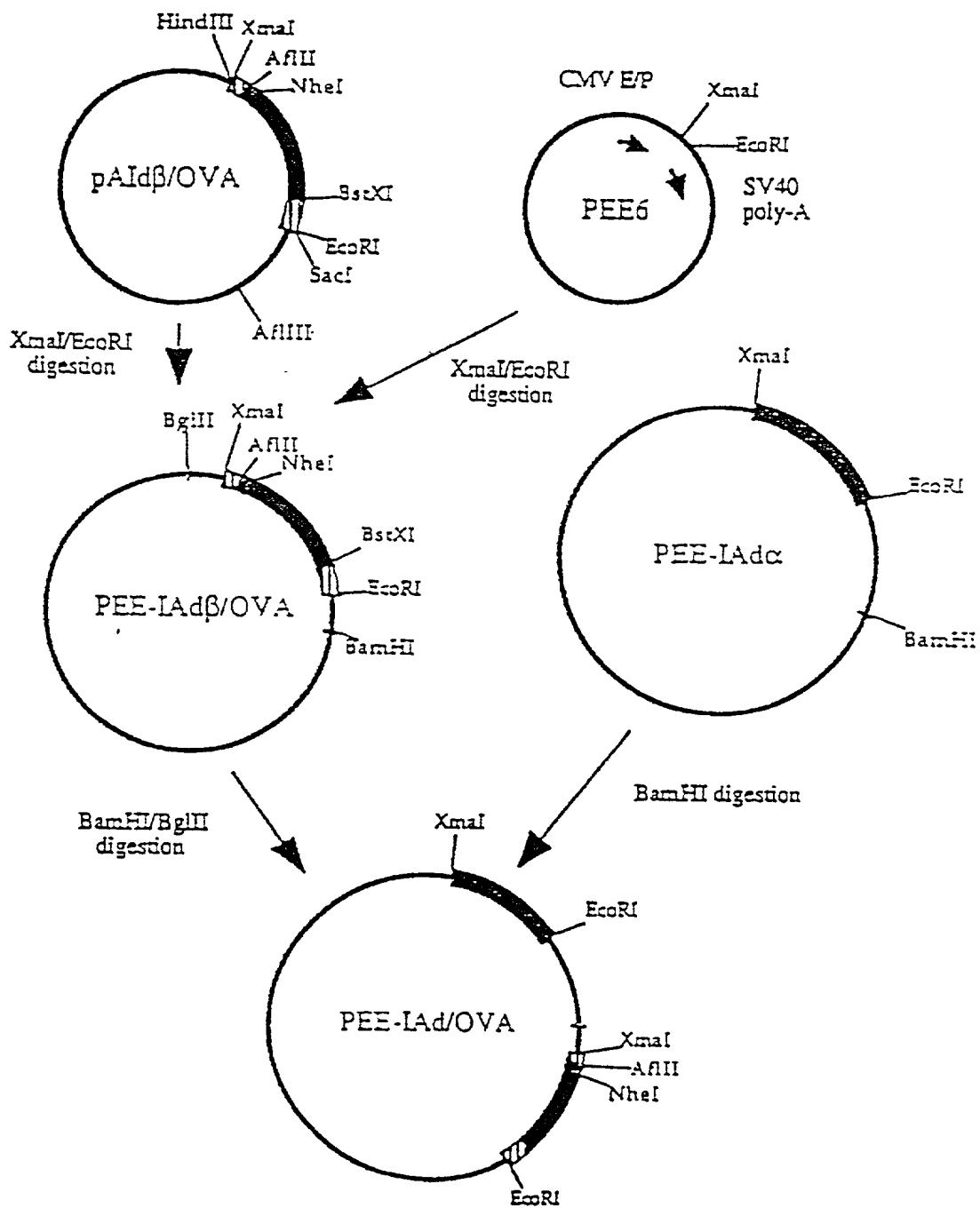


Figure 18A. Full length I-Ad α chain insert

XbaI

10	20	30	40	50
CTG AAC ACC ACG CCT TCC AGC CCT CGT ACT CCT CGG CGC CGC CGC				
CGG CGG CGC				
H P C S R A L I L G V L A				

Kozak **I-Ad α chain signal peptide**
consensus

EcoRI

60	70	80	90
CTG AAC ACC ACG CCT AGC CCT TCC CGA CCT CGA CGC CGC ATT CGC //			
CGC TCC TCC TAG GAG CGG AGC CCT CGA CCT CGT CGT TAA CGT CGT //			
L H T M L S L C G G G A Z G G I E //			

I-Ad α chain signal peptide **Signal peptide**
cleavage site

EcoRI

750	760	770	780
CGA TCA CGT CGC AGC CCT AGA CGC CGA CGG CCT TTA TCA GAA TTG			
GCT AGT CGA CGT CGC AGC CCT TCC CGT CGT CGG CGA ATT ACT CCT AAC			
R S G G T S R H P G P L *			

I-Ad α chain

Figure 18B. Full length I-Ad β chain insert

HindIII XbaI

10	20	30	40	50
AGG GGG CGG CGC AGC CCT CGT CGC CGC CGC CGC CGC CGC CGC CGC CGC				
CGG CGC CGC CGC CGC				
H A L Q I P S L L S A				

Kozak **I-Ad β chain signal peptide**
consensus

AfIII

60	70	80	90	100
GCT CGT CGT CGT AGT CGT CGT AGC AGC CGA AGC AGC AGC TTA AGT ATC				
CGA				
A V V V L M V L S S P R T C S A I				

I-Ad β chain signal peptide **Signal peptide**
cleavage site

Ova peptide

NdeI

110	120	130	140
TCT CGG CCT CGT CGC CGT CGT CGC CGT CGA ATT AAC CGA CCT CGT CGT CGT			
AGA CGA CCT CGA			
S Q A V K A A H A Z I N E A C R			

Linker region **I-Ad β chain**

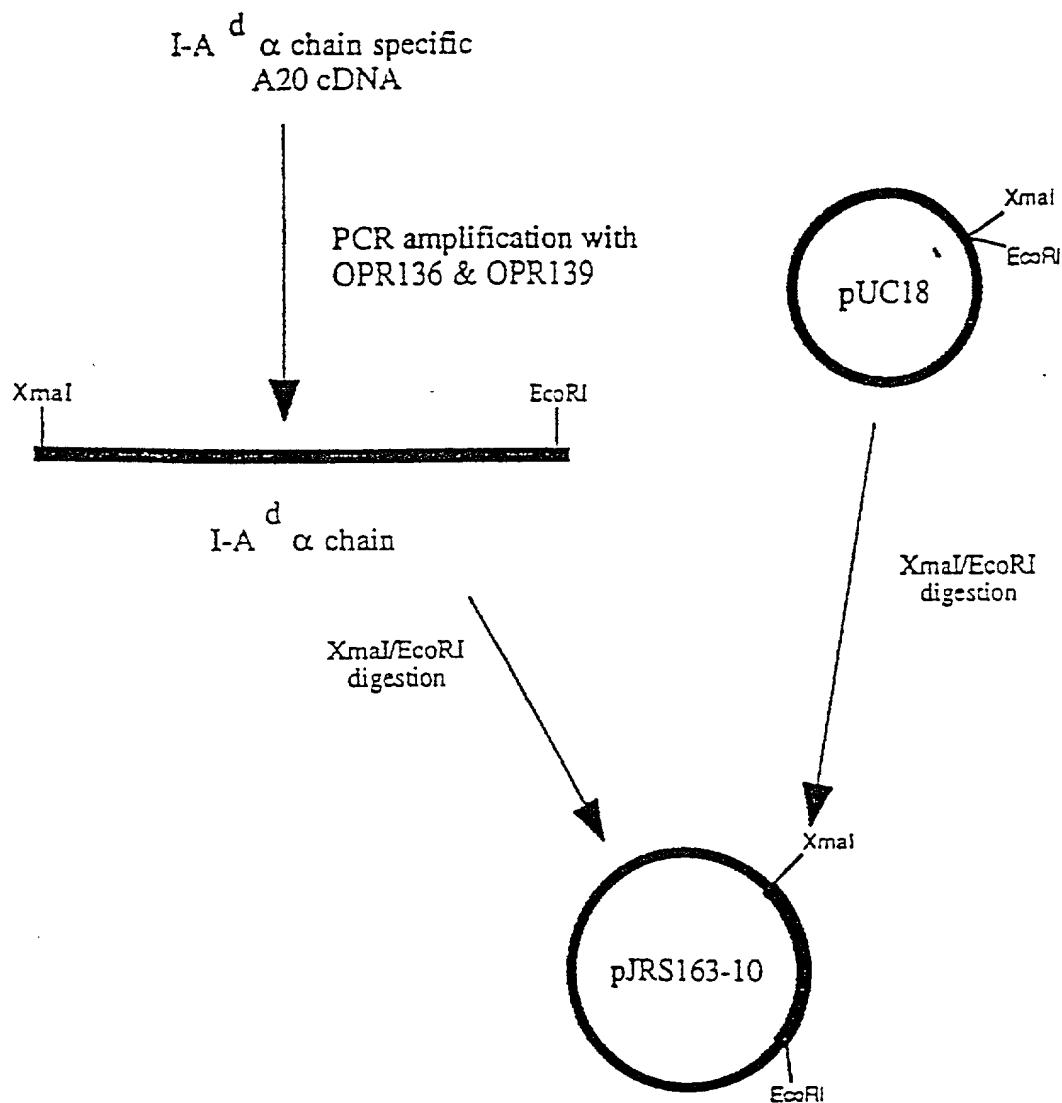
EcoRI SacI

870	880	890	900
GCT CGT CGA CGA CGG CGG CGT CGT CGC TGA CGA ATG TGC CGT CGT CGT			
CGA CGA CGA CGT			
P P P A G L L Q *			

I-Ad β chain

FIGURE 19 (Sheet 1 of 7)

Full length peptide linked MHC expression vectors



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FIGURE 19 (Sheet 2 of 7)

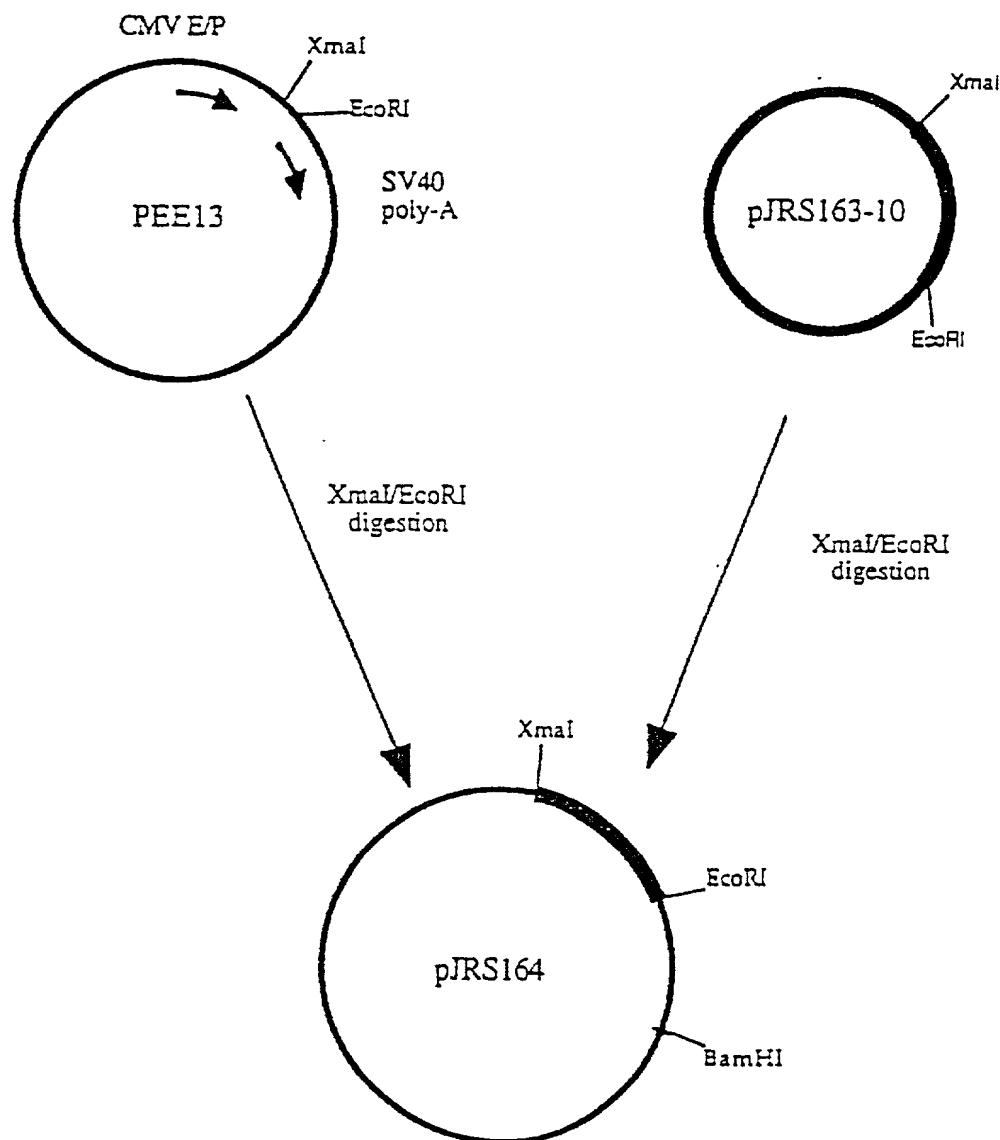
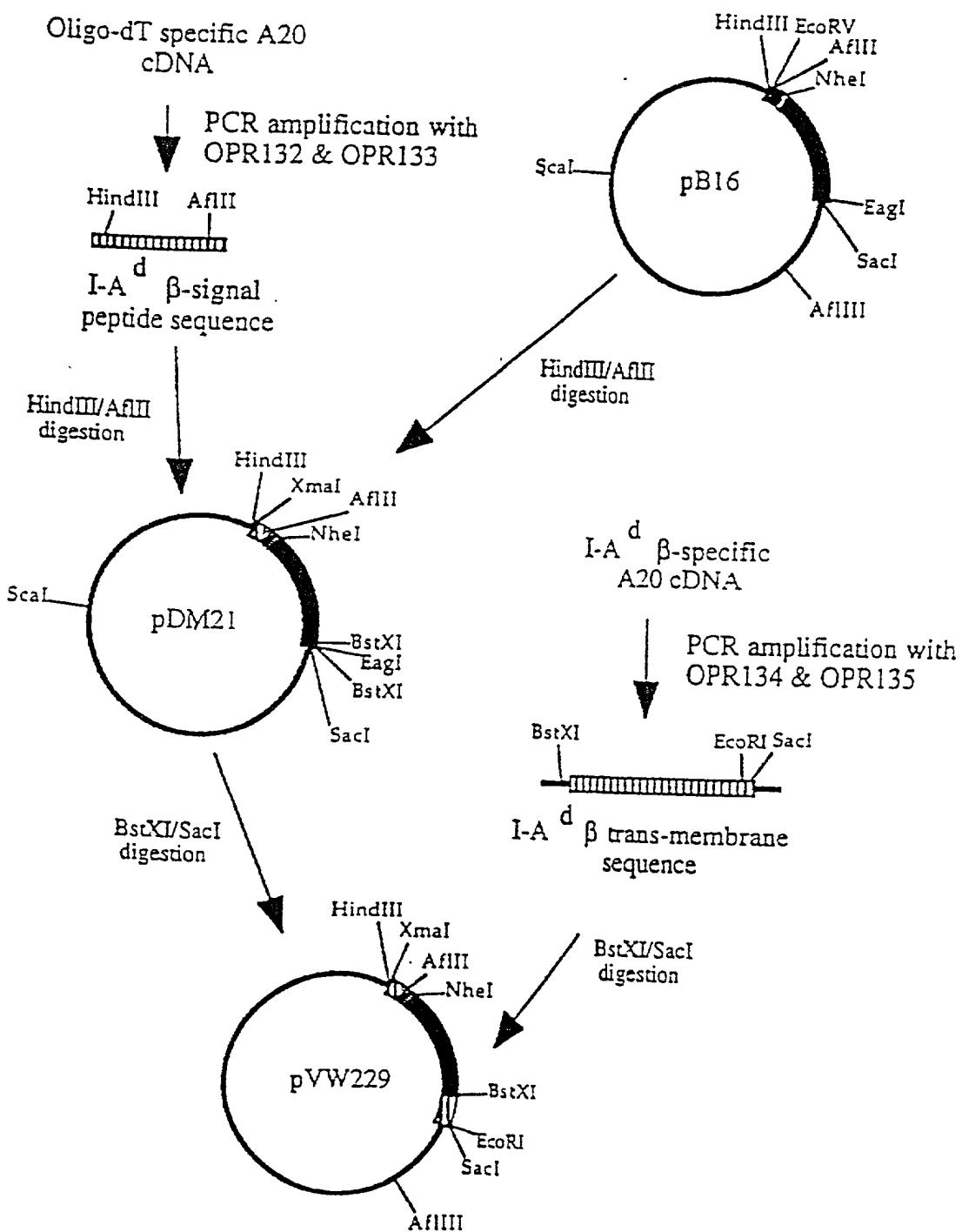
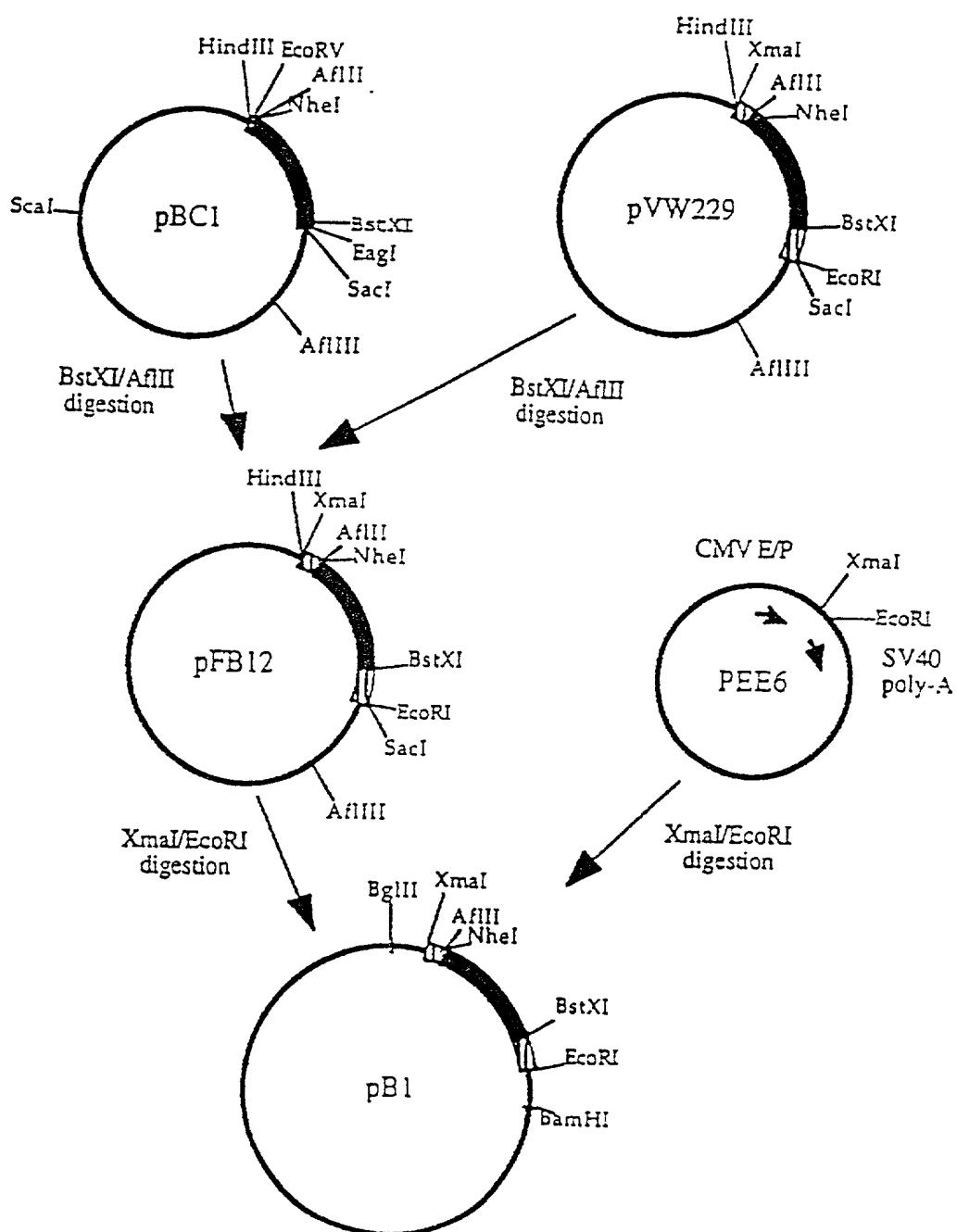


FIGURE 19 (Sheet 3 of 7)

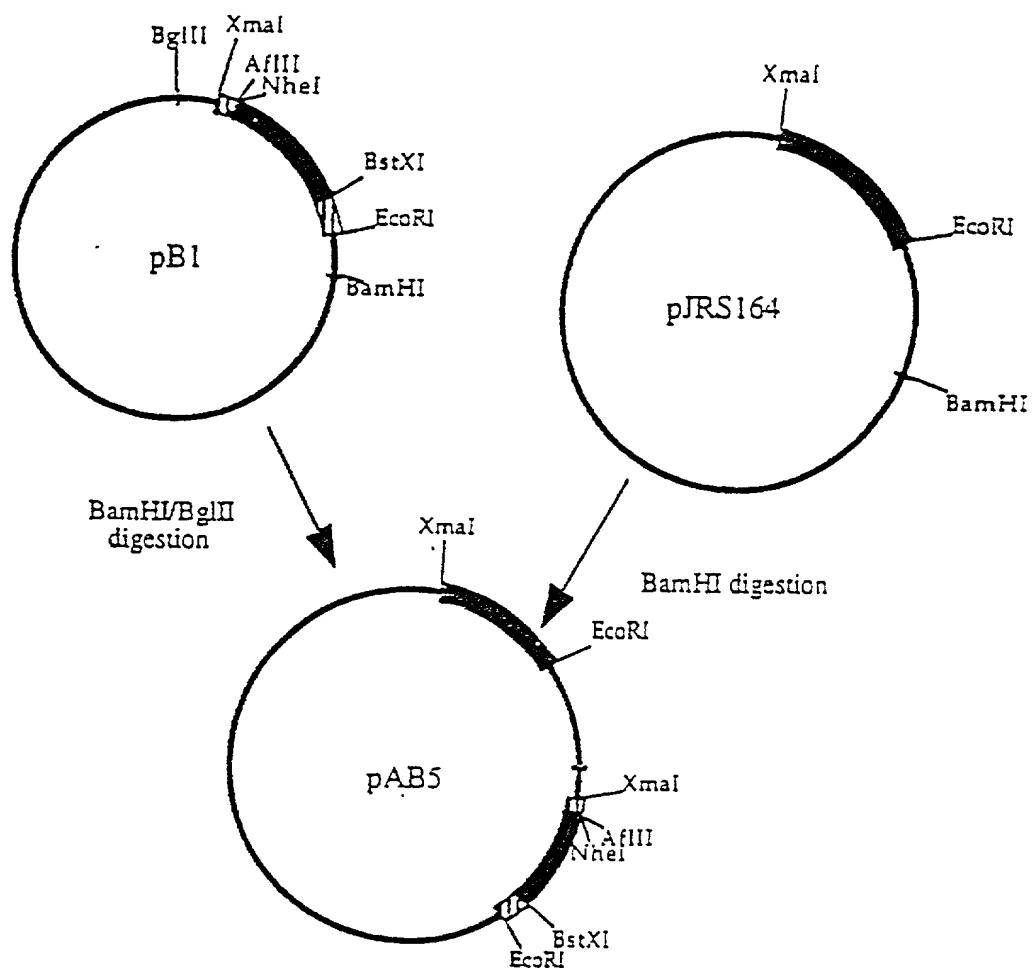


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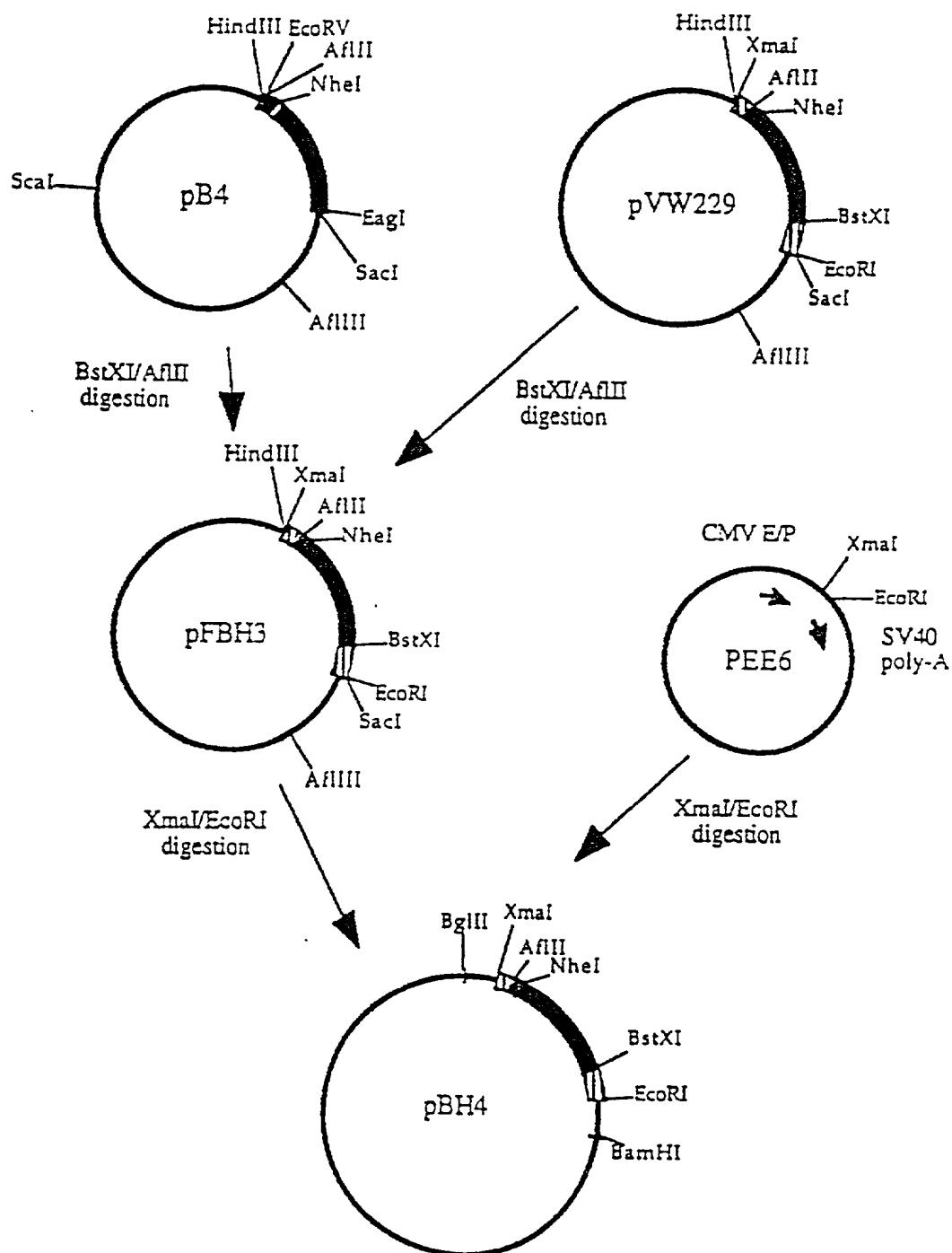
FIGURE 19 (Sheet 4 of 7)

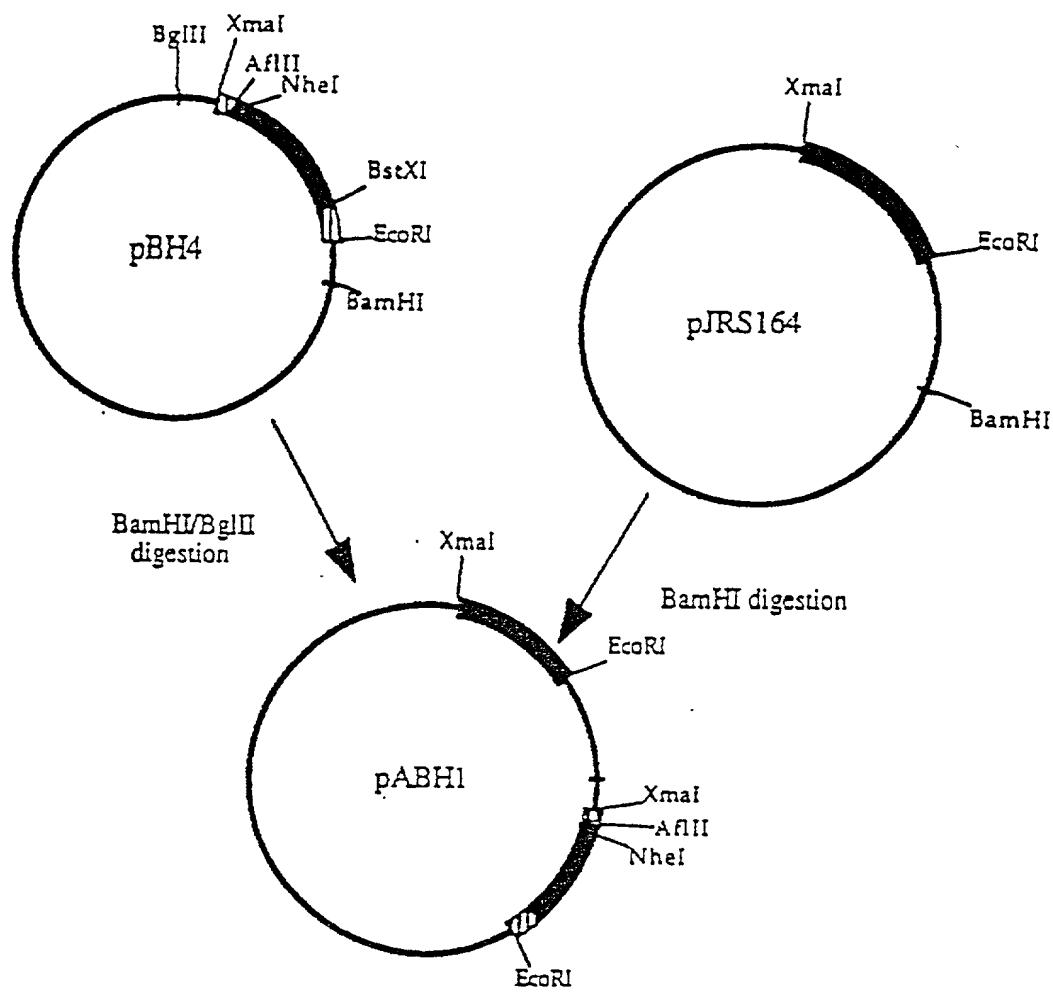


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FIGURE 19 (Sheet 5 of 7)



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FIGURE 19 (Sheet 6 of 7)



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FIGURE 19 (Sheet 7 of 7)

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FIGURE 20

Oligonucleotides used in cloning

OPR132

I-A^d β signal peptide front primer with Kozak consensus for CellTech vector -

HindIII/XbaI sites

5'-CCC CCC AAG CTT CCC GGG CCA CCA TGG CTC TGC AGA TCC CCA
GC-3'

OPR133

I-A^d β signal peptide back primer with Kozak consensus for CellTech vector - AflII site5'-CCC CCC ACT TAA GGT CCT TGG GCT GCT CAG CAC C-3'

OPR134

I-A^d β transmembrane front primer for CellTech vector - BstXI sites5'-CCC CCC CCA TCA CTG TGG AGT GGA GGG-3'

OPR135

I-A^d β transmembrane back primer for CellTech vector - SstI, EcoRI sites5'-CCC CCC GAG CTC GAA TCC TCA CTG CAG GAG CCC TGC TGG-3'

OPR136

I-A^d α signal peptide front primer with Kozak consensus for CellTech vector -

HindIII/XbaI sites

5'-CCC CCC AAG CTT CCC GGG CCA CCA TGC CGT GCA GCA GAG CTC
TG-3'

OPR139

I-A^d α transmembrane primer for CellTech vector - SstI/EcoRI sites5'-CCC CCC GAG CTC GAA TCC TCA TAA AGG CCC TGG GTG TCT G-3'

B7-1-2F

Murine B7-1 front primer with Kozak consensus for CloneTech vector - NotI site

5'-CCC CCC CCG CGG CCG CCC CAC CAT GGG ACT GAG TAA CAT TCT
C-3'

B7-1-2B

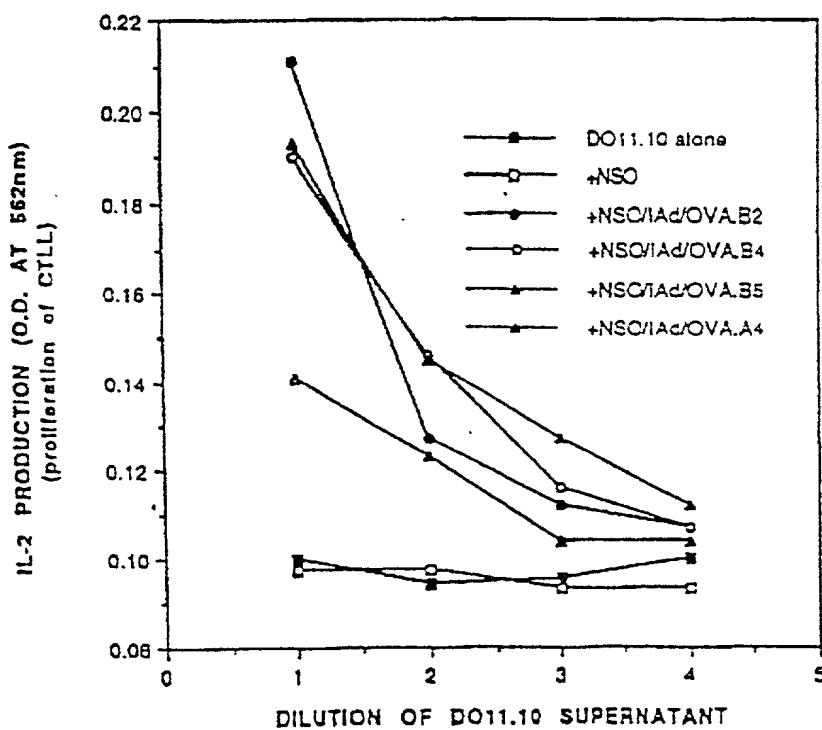
Murine B7-1 BACK primer for CloneTech vector - NotI site

5'-CCC CCC GCG GCC GCT TTA AAA ACA TGT ATC ACT TTT-3'

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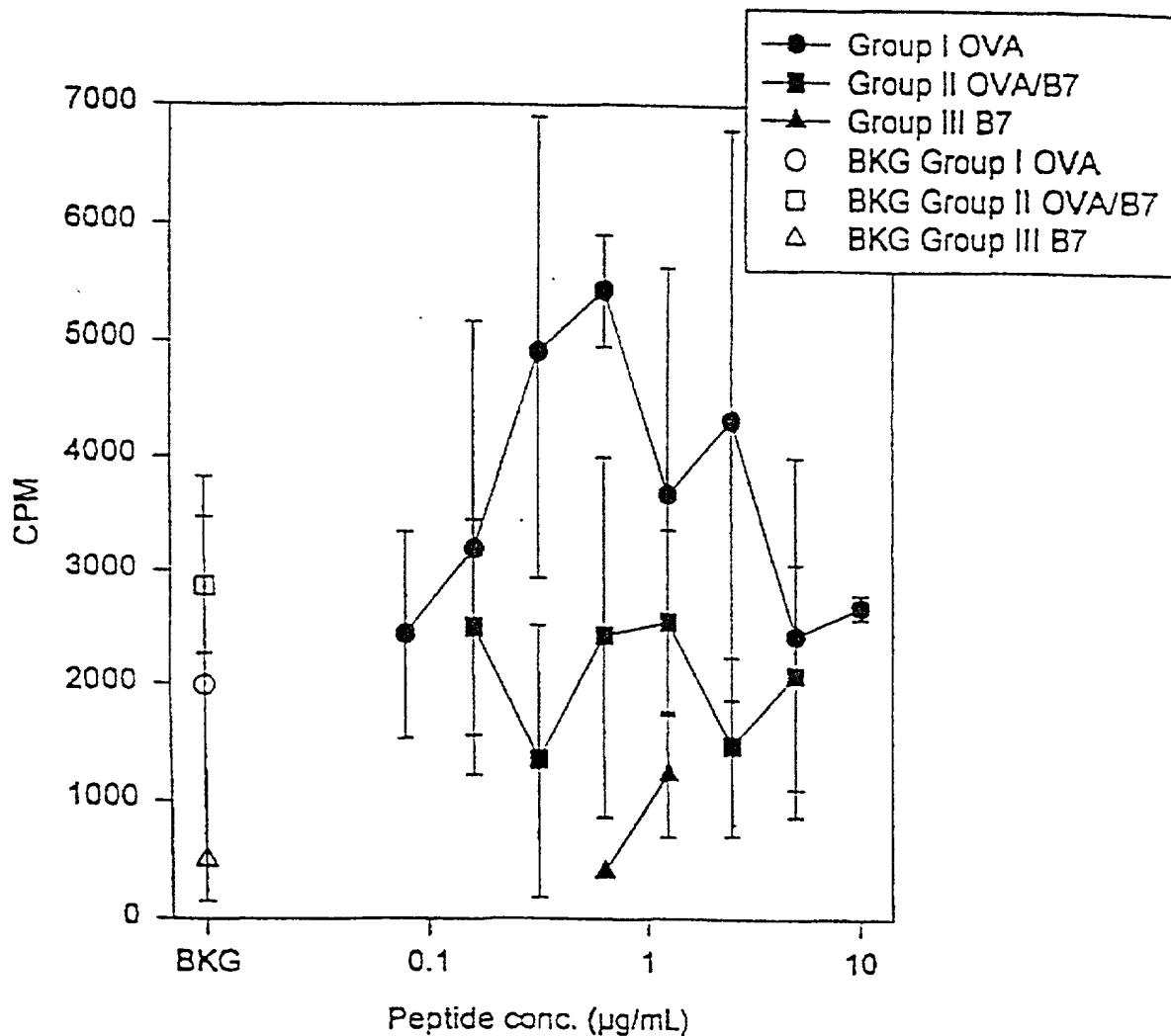
FIGURE 21

NSO/ClassII/OVA clones Stimulate IL-2 Production from DO11.10



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FIGURE 22

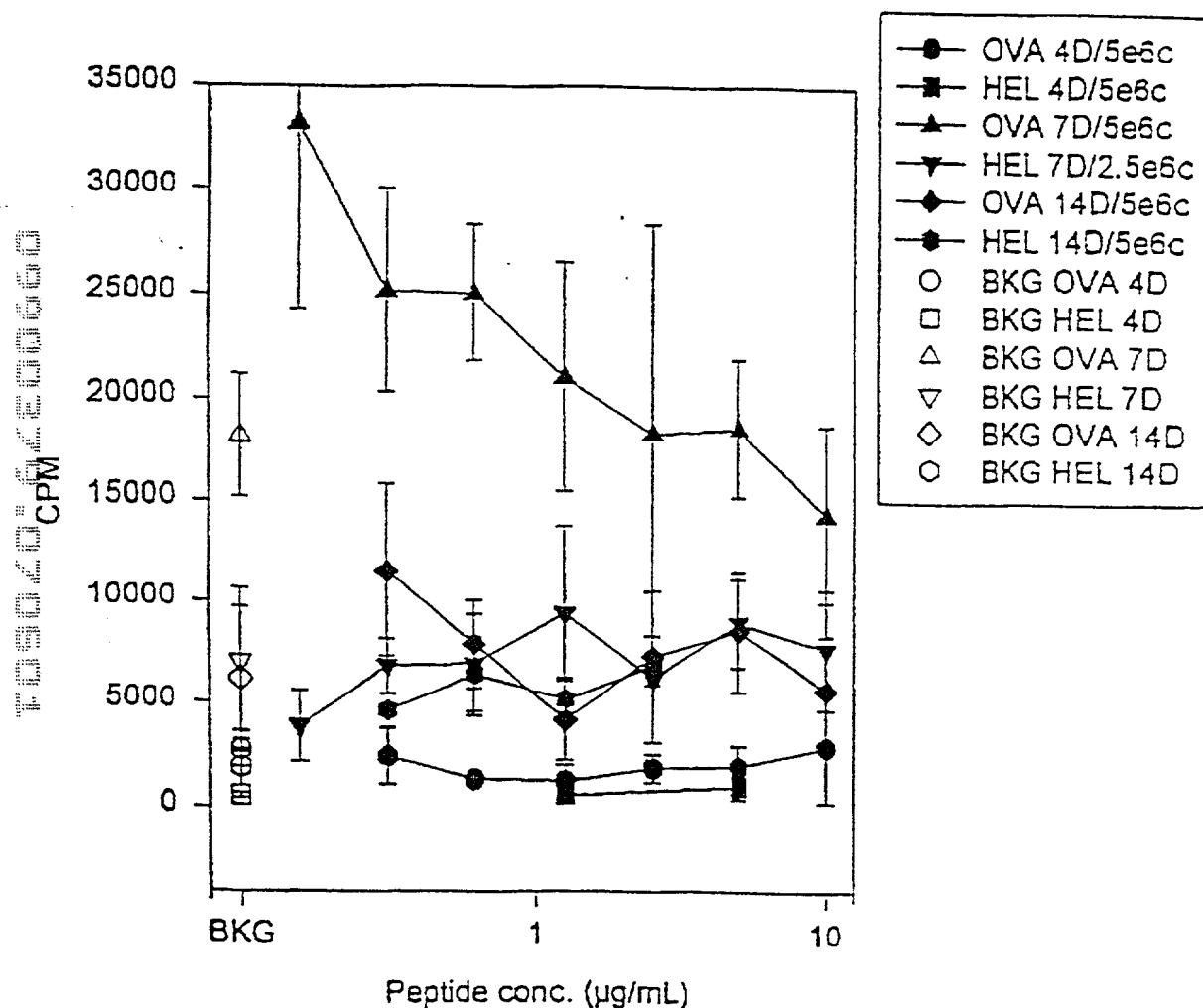
INTRAMUSCULAR IAd/OVA & B7 DNA INJECTIONS PROLIFERATION ASSAY



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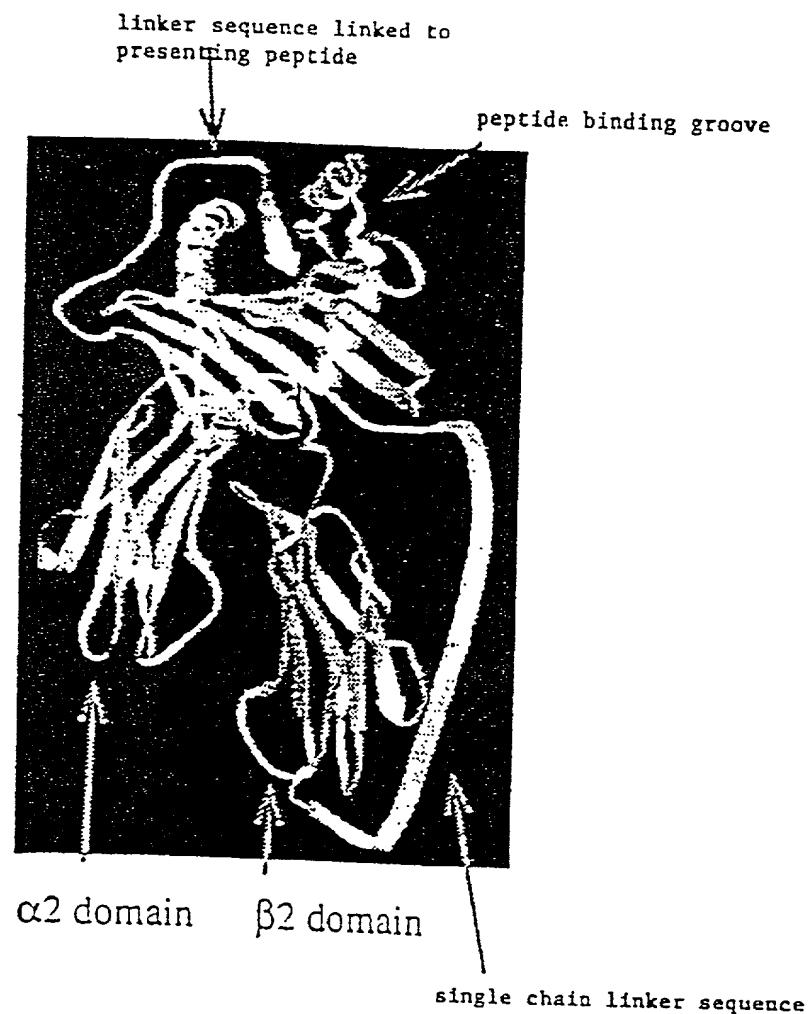
FIGURE 23

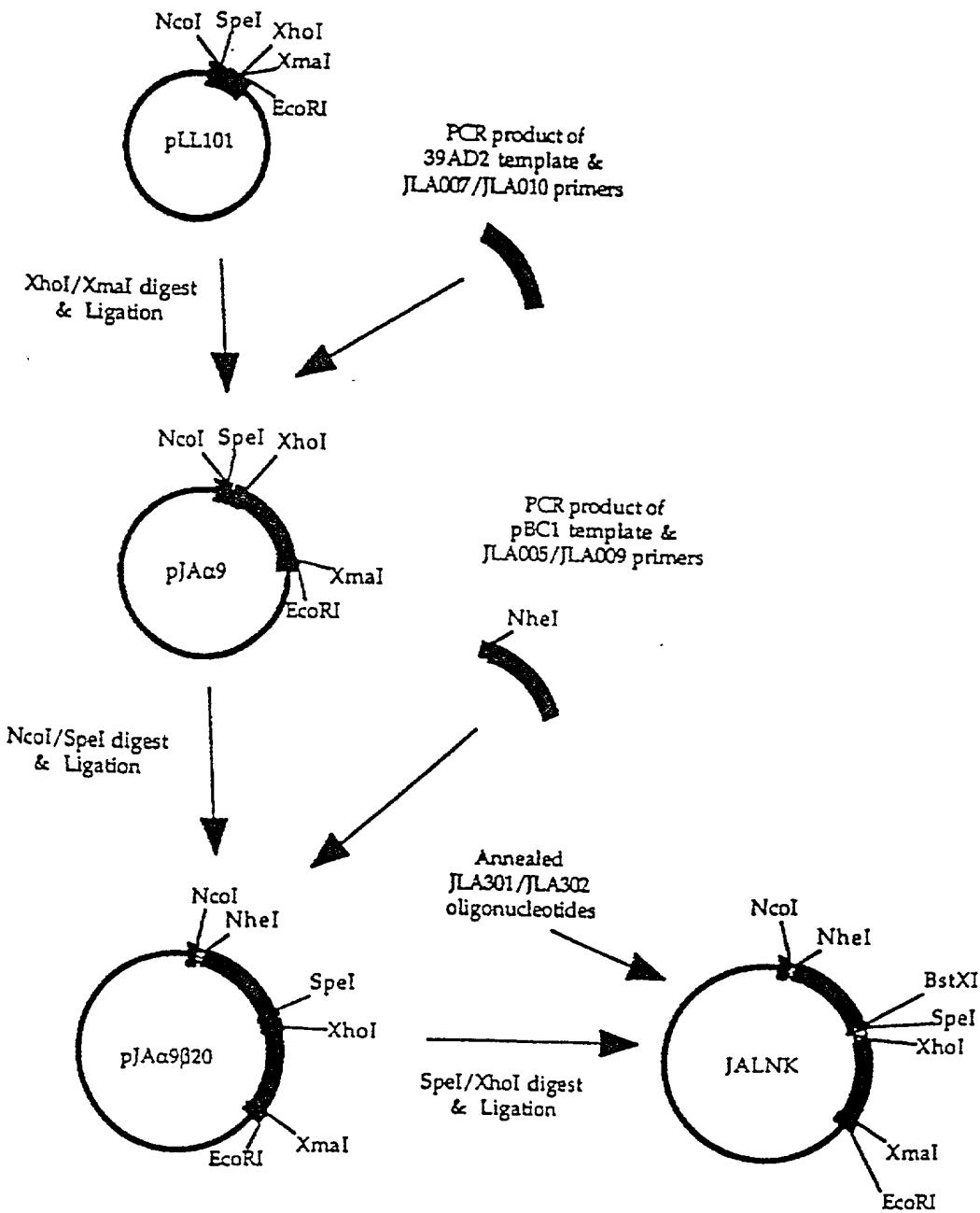
**INTRADERMAL IA_D/OVA & IA_D/HEL DNA INJECTIONS
PROLIFERATION ASSAY
4, 7 & 14 DAYS POST INJECTION**



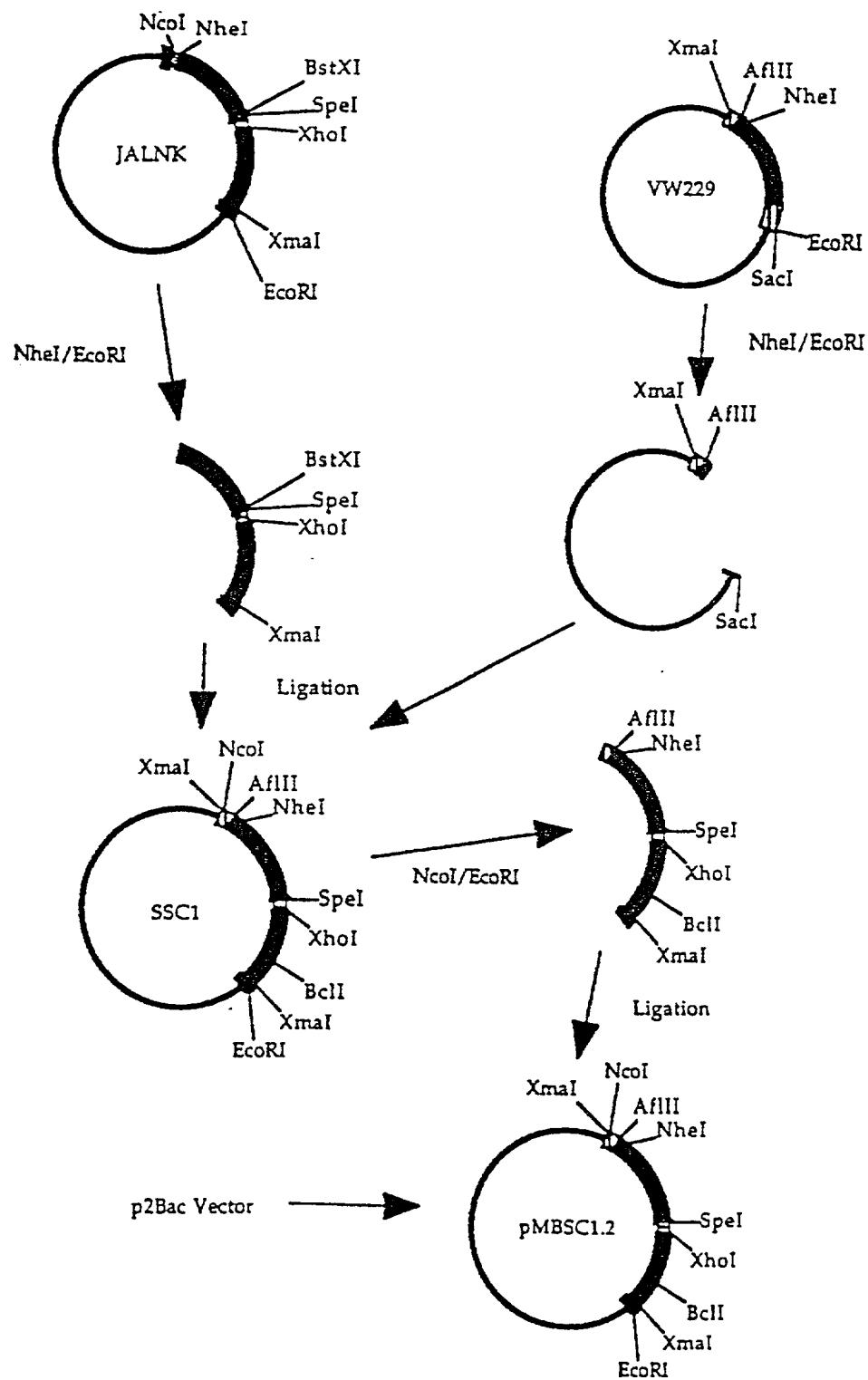
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FIGURE 24

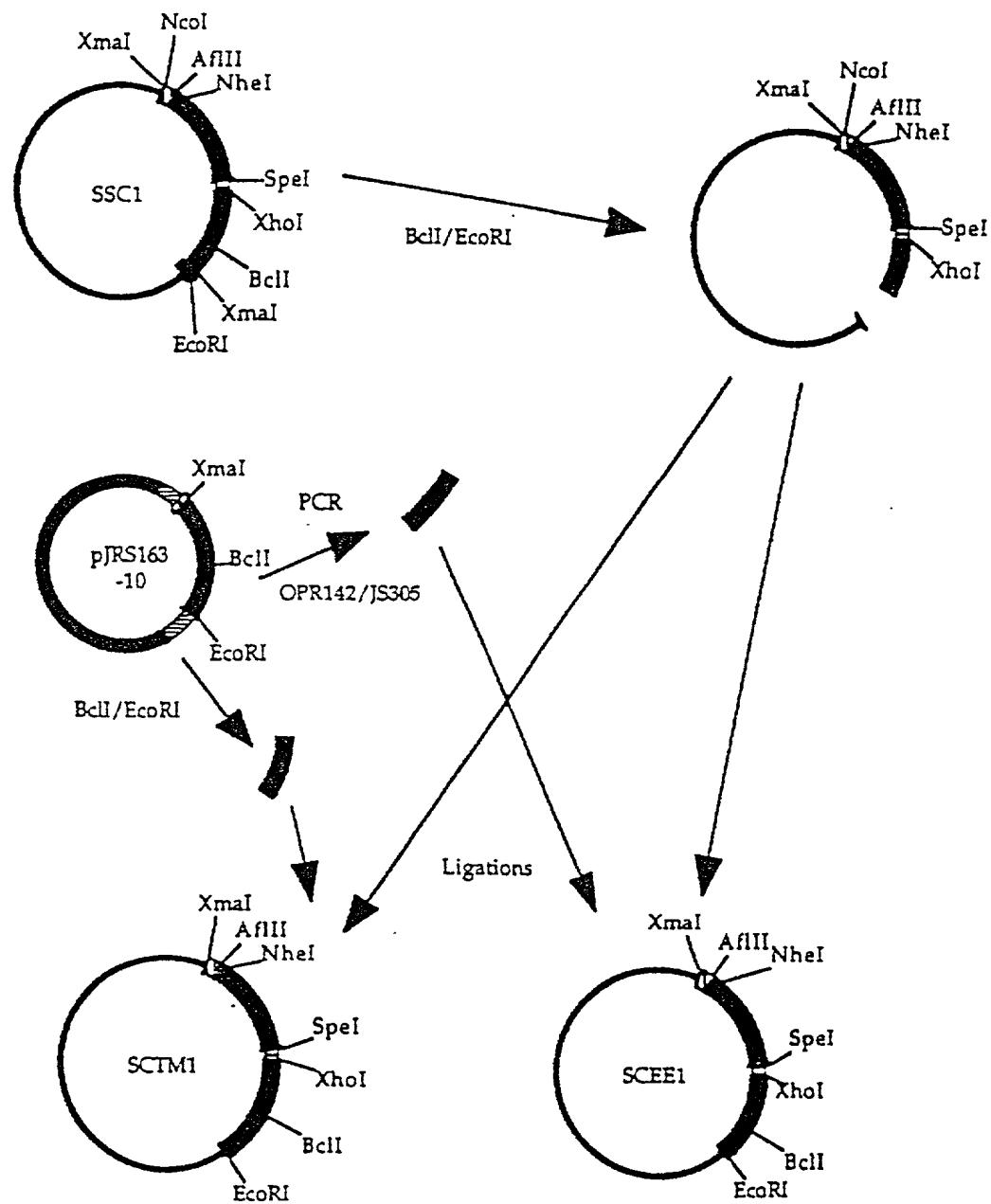


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FIGURE 25 (SHEET 1 OF 4)

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FIGURE 25 (SHEET 2 OF 4)

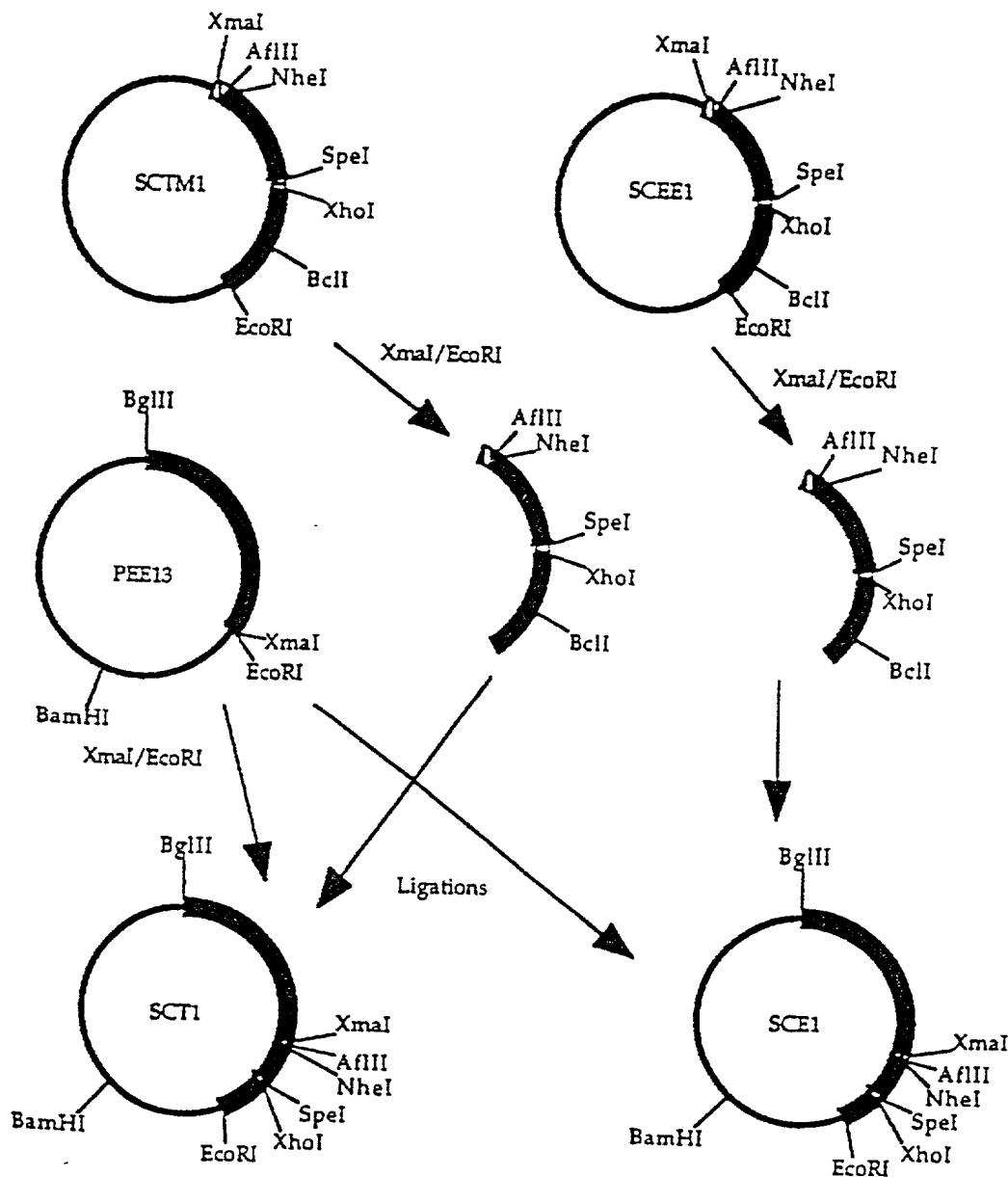


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FIGURE 25 (SHEET 3 OF 4)



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FIGURE 25 (SHEET 4 OF 4)



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FIGURE 26

JLA-005

5'-CCCCCGCCATGGCGCTAGCGGAGGGGGCGGAAGC-3'

JLA-007

5'-CCCGGGGCCTCGAGTGAAGACGACATTGAGGCCGAC-3'

JLA-009

5'-CCCCCACTAGTCCACTCCACAGTGATGGGGCT-3'

JLA-010

5'-CCCCCCCCGGGACCAGTGTTCAGAACCGGCTCCTC-3'

JLA-301

5'-TCGAGGAACCGCCACCGCCAGAACCGCCGCCACCGA-
ACCACCAACCGCCGCTGCCACCGCCACCA-3'

JLA-302

5'-CTAGTGGTGGCGGTGGCAGCGGCGGTGGTGGTCCGG-
TGGCGCGGTTCTGGCGGTGGCGGTTCC-3'

OPR-142

5'-CTTGGGAATCTGACTAAGAGG-3'

JS-305

5'-CAGGTCGAATTCTCATCCATGGCATGTAACCTTCTT-
CCTCCCAGTGTTCAGAACCGG-3'

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FIGURE 27 (SHEET 1 OF 4)

10 20 30 40 50

CCACC ATG GCT CTG CAG ATC CCC AGC CTC CTC CTC TCA GCT GCT GTG GTG
GGTGG TAC CGA GAC GTC TAG GGG TCG GAG GAG AGT CGA CGA CAC CAC
M A L Q I P S L L L S A A V V>
----- I-Ad β chain leader -----

60 70 80 90

GTG CTG ATG GTG CTG AGC AGC CCA AGC ACC TTA AGT ATC TCT CAG GCT
CAC GAC TAC CAC GAC TCG TCG GGT TCC TGG AAT TCA TAG AGA GTC CGA
V L M V L S S P R T L S I S Q A>
-----><-----

100 110 120 130 140

GTT CAC GCT GCT CAC GCT GAA ATC AAC GAA GCT GGT CGT GCT ACC CGA
CAA GTG CGA CGA GTG CGA CTT TAG TTG CTT CGA CCA CGA CGA TCG CCT
V H A A H A E I N E A G R A S G>
----- OVA 323-339 -----><-----

150 160 170 180 190

GGG GGC GGA AGC GGC GGA GGG GGA AAC TCC GAA AGG CAT TTC GTG GTC
CCC CGG CCT TCG CCG CCT CCC CCT TTG AGG CTT TCC GTC AAG CAC CAG
G G G S G G G N S E R H F V V>
-- 10 amino acid linker --><----- I-Ad β -1 domain -----

200 210 220 230 240

CAG TTC AAG GGC GAG TCC TAC TAC ACC AAC GGG ACG CAG CGC ATA CGG
GTC AAG TTC CCG CTC ACC ATG ATG TGG TTG CCC TCC GTC GCG TAT GCC
Q F K G E C Y Y T N G T Q R I R>

250 260 270 280 290

CTC GTG ACC AGA TAC ATC TAC AAC CGG GAG GAG TAC GTG CGC TAC GAC
GAG CAC TGG TCT ATG TAG ATG TTG GCC CTC CTC ATG CAC GCG ATG CTC
L V T R Y I Y N R E E Y V R Y D>

300 310 320 330

AGC GAC GTG GGC GAG TAC CGC GGG GTG ACC GAG CTG GGG CGG CCA GAC
TCC CTC CAC CGG CTC ATG GCG CGC CAC TGG CTC GAC CCC CGC GGT CTG
S D V G E Y R A V T E L G R P D>

340 350 360 370 380

GCC GAG TAC TGG AAC ACC CAG CGG GAG ATC CTC GAG CGA AGC CGG GCC
CGG CTC ATG ACC TTG TCG GTC CGC CTC TAG GAC CTC GCT TGC GCC CGG
A E Y W N S Q P E I L E R T R A>

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FIGURE 27 (SHEET 2 OF 4)

390 400 410 420 430

GAG GTG GAC ACG GCG TGC AGA CAC AAC TAC GAG GGG CCG GAG ACC AGC
CTC CAC CTG TGC CCC ACG TCT GTG TTG ATG CTC CCC CCC CTC TGG TCG
E V D T A C R H N Y E G P E T S>

440 450 460 470 480

ACC TCC CTG CGG CGG CTT GAA CAG CCC AAT GTC GCC ATC TCC CTG TCC
TGG AGG GAC CCC GCC GAA CTT GTC GGG TTA CAG CGG TAG AGG GAC AGG
T S L R R L E Q P N V A I S L S>

--- I-Ad β -1 domain ->----- I-Ad β -2 domain -----

490 500 510 520 530

AGG ACA GAG GCG CTC AAC CAC AAC ACT CTG GTC TGT TCG GTG ACA
TCC TGT CTC CGG GAG TTG GTG GTC TTG TGA GAC CAG ACA AGC CAC TGT
R T E A L N H H N T L V C S V D>

540 550 560 570

GAT TTC TAC CCA GCC AAG ATC AAA GTG CCC TGG TTC AGG AAT GGC CAG
CTA AAG ATG GGT CGG TTC TAG TTT CAC CCC ACC AAG TCC TTA CCG GTC
D F Y P A K I K V R W F R N G Q>

580 590 600 610 620

GAG GAG ACA GTG GGG GTC TCA TCC ACA CAG CTT ATT AGG AAT GGG GAC
CTC CTC TGT CAC CCC CAG AGT AGG TGT GTC GAA TAA TCC TTA CCC CTG
E E T V G V S S T Q L I R N G D>

630 640 650 660 670

TGG ACC TTC CAG GTC CTG GTC ATG CTG GAC ATG ACC CCT CAT CAG GGA
ACC TGG AAG GTC CAG GAC CAG TAC GAC CTC TAC TGG CGA GTA GTC CCT
W T F Q V L V M L E H T P H Q G>

680 690 700 710 720

GAG GTC TAC ACC TGC CAT GTG GAG CAT CCC AGC CTG AAG ACC CCC ATC
CTC CAG ATG TGC ACC GTA CAC CTC GTA GGG TCG GAC TTC TCG GGG TAG
E V Y T C H V E H P S L K S P I>

--- I-Ad β -2 domain -----

730 740 750 760 770

ACT GTG GAG TGG ACT AGT GGT GGC CCT GGC AGC GGC GGT GGT GGT TCC
TGA CAC CTC ACC TGA TCA CCA CCA CCG CCA CCG CCA CCA CCA AGC
T V E W T S G G G G S G G G G G S>

---><----- 24 amino acid linker -----

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FIGURE 27 (SHEET 3 OF 4)

780 790 800 810

GGT GGC GGC GGT TCT GGC GGT TCC TGG ACT GAA GAC GAC ATT
 CCA CCG CCG CCA AGA CCG CCA CCG CCA AGG AGC TCA CTT CTG CTG TAA
 G G G G S G G G S S S E D D I>
 -----><-----

820 830 840 850 860

GAG GCC GAC CAC GTA GGC TTC TAT GGT ACA ACT GTT TAT CAG TCT CCT
 CTC CGG CTG GTG CAT CCG AAG ATA CCA TGT TGA CAA ATA GTC AGA GGA
 E A D H V G F Y G T T V Y Q S P>
 ----- I-Ad α -1 domain -----

870 880 890 900 910

GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT GAT GAG TTC TTC
 CCT CTG TAA CCG GTC ATG TGT GTA CTT AAA CTA CCA CTA CTC AAC AAG
 G D I G Q Y T H E F D G D E L F>

920 930 940 950 960

TAT GTG GAC TTG GAT AAG AAG AAA ACT GTC TGG AGG CTT CCT GAG TTT
 ATA CAC CTG AAC CTA TTC TTC TTT TGA CAG ACC TCC GAA GGA CTC AAA
 Y V D L D K K K T V W R L P E F>

970 980 990 1000 1010

GCG CAA TTG ATA CTC TTT GAG CCC CAA GGT GGA CTG CAA AAC ATA GCT
 CCG GTT AAC TAT GAG AAA CTC GGG GTT CCA CCT GAC GTT TTG TAT CGA
 G Q L I L F E P Q G G L Q N I A>

1020 1030 1040 1050

GCA GAA AAA CAC AAC TTG GGA ATC TTG ACT AAG AGG TCA AAT TTC ACC
 CGT CTT TTT GTG TTG AAC CCT TAG AAC TGA TTC TCC AGT TTA AAG TGG
 A E K H N L G I L T K R S N F T>
 ----- I-Ad α -1 domain -----

1060 1070 1080 1090 1100

CCA GCT ACC AAT GAG GGT CCT CAA GCG ACT GTG TTC CCC AAG TCC CCT
 GGT CGA TGG TTA CTC CGA CGA GTT CGC TGA CAC AAG GGG TTC AGG GGA
 P A T N E A P Q A T V F P K S P>
 -----><----- I-Ad α -2 domain -----

1110 1120 1130 1140 1150

GTG CTG CTG GGT CAG CCC AAC ACC CTT ATC TGC TTT GTG GAC AAC ATC
 CAC GAC GAC CCA GTC GGG TTG TGG GAA TAG AGC AAA CAC CTG TTG TAG
 V L L G Q P N T L I C F V D N I>

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FIGURE 27 (SHEET 4 OF 4)

1160	1170	1180	1190	1200
<pre> TTC CCT CCT GTG ATC AAC ATC ACA TGG CTC AGA AAT AGC AAG TCA GTC AAG GGT GGA CAC TAG TTG TAG TGT ACC GAG TCT TTA TCG TTC AGT CAG F P P V I N I T W L R H S K S V> -----</pre>				
1210	1220	1230	1240	1250
<pre> ACA GAC GGC GTT TAT GAG ACC AGC TTC CTC GTC AAC CGT GAC CAT TCC TGT CTG CCG CAA ATA CTC TGG TCG AAG GAG CAG TTG GCA CTG GTA AGG T D G V Y E T S F L V N R D E S> -----</pre>				
1260	1270	1280	1290	
<pre> TTC CAC AAG CTG TCT TAT CTC ACC TTC ATC CCT TCT GAT GAT GAC ATT AAG GTG TTC GAC AGA ATA GAG TGG AAG TAG CGA AGA CTA CTA CTG TAA F H K L S Y L T F I P S D D D I> -----</pre>				
1300	1310	1320	1330	1340
<pre> TAT GAC TGC AAG GTG GAG CAC TGG CCC CTG GAG GAG CCG GTT CTG AAA ATA CTG ACC TTC CAC CTC GTG ACC CCC GAC CTC CTC CCC CAA GAC TTT Y D C K V E H W G L E E P V L K> ----- I-Ad α-2 domain -----</pre>				
1350	1360	1370	1380	
<pre> CAC TGG TCC CGG CCT AGT CAC CAT CAC CAT CAC TAG GTG ACC AGG CCC CGA TCA GTG GTA GTG GTA GTG ATC H W S R A S H H H H H H H H *-> -----><----- 6 X HIS tag -----></pre>				

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FIGURE 28 (SHEET 1 OF 4)

10	20	30	40	50
CCACC ATG CCT CTG CAG ATC CCC AGC CTC CTC CTC TCA GCT GCT GTG GTG GGTCG TAC CGA GAC GTC TAG GGG TCG GAG GAG ACT CGA CGA CAC CAC M A L Q I P S L L L S A A V V> <----- I-Ad β chain leader ----->				
60	70	80	90	
GTC CTG ATG GTG CTG AGC AGC CCA AGG ACC TTA ACT ATC TCT CAG GCT CAC GAC TAC CAC GAC TCG TCG GGT TCC TGG AAT TCA TAG AGA GTC CGA V L M V L S S P R T L S I S Q A> ----->				
100	110	120	130	140
GTT CAC CCT GCT CAC GCT GAA ATC AAC GAA GCT GGT CGT GCT AGC GGA CAA GTG CGA CGA GTG CGA CTT TAG TTG CTT CGA CCA GCA CGA TCG CCT V H A A H A E I N E A G R A S G> ----- OVA 323-339 ----->				
150	160	170	180	190
GGG GGC GGA AGC GGC GGA GGG GGA AAC TCC GAA AGG CAT TTC GTG GTC CCC CCG CCT TCG CCG CCT CCC CCT TTG AGG CTT TCC GTA AAG CAC CAG G G G S G G G N S E R H F V V> -- 10 amino acid linker --><----- I-Ad β -1 domain ----->				
200	210	220	230	240
CAG TTC AAG GGC GAG TGC TAC TAC ACC AAC GGG AGC CAG CGC ATA CGG GTC AAG TTC CCG CTC ACG ATG ATG TGG TTG CCC TGC GTC GCG TAT GCC Q F K G E C Y Y T N G T Q R I R> ----->				
250	260	270	280	290
CTC GTG ACC AGA TAC ATC TAC AAC CGG GAG GAG TAC GTG CGC TAC GAC GAG CAC TGG TCT ATG TAG ATG TTG CCC CTC CTC ATG CAC GCG ATG CTG L V T R Y I Y N R E E Y V R Y D> ----->				
300	310	320	330	
AGC GAC GTG GGC GAG TAC CGC GCG GTG ACC GAG CTG GGG CGG CGG CCA GAC TCG CTG CAC CGG CTC ATG GCG CGC CAC TGG CTC GAC CCC GCG GGT CTG S D V G E Y R A V T E L G R P D> ----->				
340	350	360	370	380
GCC GAG TAC TGG AAC ACC CAG CGG GAG ATC CTG GAG CGA ACG CGG GGC CGG CTC ATG ACC TTG TCG GTC GGC CTC TAG GAC CTC CCT TGC GCC CGG A E Y W N S Q P E I L E R T R A> ----->				

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FIGURE 28 (SHEET 2 OF 4)

390 400 410 420 430

GAG GTG GAC ACG GCG TGC AGA CAC AAC TAC GAG GGG CCG GAG ACC AGC
CTC CAC CTG TGC CGC ACG TCT GTG TTG ATG CTC CCC GGC CTC TGG TCG
E V D T A C R H N Y E G P E T S>

440 450 460 470 480

ACC TCC CTG CGG CGG CTT GAA CAG CCC AAT GTC CCC ATC TCC CTG TCC
TGG AGG GAC GCC GCC GAA CTT GTC GGG TTA CAG CGG TAG AGG GAC AGG
T S L R R L E Q P N V A I S L S>

--- I-Ad β -1 domain ->--- I-Ad β -2 domain -----

490 500 510 520 530

AGG ACA GAG GCC CTC AAC CAC CAC AAC ACT CTC GTC TGT TCG TCG ACA
TCC TGT CTC CGG GAG TTG GTG GTG TTG TGA GAC CAG ACA AGC CAC TGT
R T E A L N H H N T L V C S V T>

540 550 560 570

GAT TTC TAC CCA GCC AAG ATC AAA GTG CGC TGG TTC AGG AAT GGC CAG
CTA AAG ATG GGT CGG TTC TAG TTT CAC CGG ACC AAG TCC TTA CCG GTC
D F Y P A K I K V R W F R N G Q>

580 590 600 610 620

GAG GAG ACA GTG GGG GTC TCA TCC ACA CAG CTT ATT AGG AAT GGG GAC
CTC CTC TGT CAC CCC CAG AGT AGG TGT GTC GAA TAA TCC TTA CCC CTC
E E T V G V S S T Q L I R N G D>

630 640 650 660 670

TGG ACC TTC CAG GTC CTG GTC ATG CTG GAG ATG ACC CCT CAT CAG CGA
ACC TCG AAG GTC CAG GAC CAG TAC GAC CTC TAC TCG CGA GTA GTC CCT
W T F Q V L V M L E M T P H Q G>

680 690 700 710 720

GAG GTC TAC ACC TGC CAT GTG GAG CAT CCC ACC CTG AAG ACC CCC ATC
CTC CAG ATG TCG ACC GTA CAC CTC GTC GCA CGG TCG GAC TTC TCG GGG TAG
E V Y T C H V E H P S L K S P I>

--- I-Ad β -2 domain -----

730 740 750 760 770

ACT GTG GAG TGG ACT AGT GGT GGC GGT GGC AGC GGC GGT GGT GGT TCC
TCA CAC CTC ACC TGA TCA CCA CGG CCA CGG TCG CGG CCA CCA CCA AGG
T V E W T S G G G S G G G G G S>

-----><----- 24 amino acid linker -----

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FIGURE 28 (SHEET 3 OF 4)

780 790 800 810
 CCT GGC GGC GGT TCT GGC GGT GGT TCC TCG AGT GAA GAC GAC ATT
 CCA CCG CCG CCA AGA CCG CCA CCG CCA AGG AGC TCA CTT CTG CTG TAA
 G G G G S G G G S S S S E D D I>
 -----><-----
 820 830 840 850 860
 GAG GGC GAC CAC GTA GGC TTC TAT GGT ACA ACT GTT TAT CAG TCT CCT
 CTC CCG CTG GTG CAT CCG AAG ATA CCA TGT TGA CAA ATA GTC AGA GGA
 E A D H V G F Y G T T V Y Q S P>
 ----- I-Ad α -1 domain -----
 870 880 890 900 910
 GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT CAT GAG TTG TTC
 CCT CTG TAA CCG GTC ATG TGT GTA CTT AAA CTA CCA CTA CTC AAC AAG
 G D I G Q Y T H E F D G D E L F>

 920 930 940 950 960
 TAT GTG GAC TTG GAT AAG AAG AAA ACT GTC TCG AGG CTT CCT GAG TTT
 ATA CAC CTG AAC CTA TTC TTC TTT TGA CAG ACC TCC GAA GGA CTC AAA
 Y V D L D K K T V W R L P E F>

 970 980 990 1000 1010
 GGC CAA TTG ATA CTC TTT GAG CCC CAA GGT GGA CTG CAA AAC ATA GCT
 CCG GTT AAC TAT GAG AAA CTC GGG GTT CCA CCT GAC GTT TTG TAT CGA
 G Q L I L F E P Q G G E Q N I A>

 1020 1030 1040 1050
 GCA GAA AAA CAC AAC TTG GGA ATC TTG ACT AAG AGG TCA ATT TTC ACC
 CGT CTT TTT GTG TTG AAC CCT TAG AAC TGA TTC TCC ACT TTA AAG TGG
 A E K H N L G I L T K R S N F T>
 ----- I-Ad α -1 domain -----
 1060 1070 1080 1090 1100
 CCA GCT ACC AAT GAG GGT CCT CAA GCG ACT GTG TTC CCC AAG TCC CCT
 GGT CGA TGG TTA CTC CGA GGA GTT CGC TGA CAC AAG GGG TTC AGG GGA
 P A T N E A P Q A T V F P K S P>
 -----><----- I-Ad α -2 domain -----
 1110 1120 1130 1140 1150
 GTG CTG CTG GGT CAG CCC AAC ACC CTT ATC TGC TTT GTG GAC AAC ATC
 CAC GAC GAC CCA GTC GGG TTG TGG GAA TAG ACG AAA CAC CTG TTG TAG
 V L L G Q P N T L I C F V D N I>

FIGURE 28 (SHEET 4 OF 4)

1160 1170 1180 1190 1200

TTC CCT CCT GTG ATC AAC ATC ACA TGG CTC AGA AAT AGC AAG TCA GTC
 AAC GGT GGA CAC TAG TTC TAG TGT ACC GAG TCT TTA TCG TTC AGT CAG
 F P P V I N I T W L R N S K S V>

1210 1220 1230 1240 1250

ACA GAC GGC GTT TAT GAG ACC AGC TTC CTC GTC AAC CGT GAC CAT TCC
 TGT CTG CCG CAA ATA CTC TGG TCG AAG GAG CAG TTG GCA CTG GTA AGG
 T D G V Y E T S F L V N R D H S>

1260 1270 1280 1290

TTC CAC AAG CTG TCT TAT CTC ACC TTC ATC CCT TCT GAT GAT GAC ATT
 AAG GTG TTC GAC AGA ATA GAG TGG AAG TAG GGA AGA CTA CTA CTG TAA
 F H K L S Y L T F I P S D D D I>

1300 1310 1320 1330 1340

TAT GAC TGC AAG GTG GAG CAC TGG CCC CTG GAG GAG CCG GTT CTC AAA
 ATA CTG ACC TTC CAC CTC GTG ACC CCG GAC CTC CTC GGC CAA GAC TTT
 Y D C K V E H W G L E E P V L K>

----- I-Ad α -2 domain -----

1350 1360 1370 1380 1390

CAC TGG GAA CCT GAG ATT CCA GGC CCC ATG TCA GAG CTG ACA GAA ACT
 GTG ACC CTT GGA CTC TAA GGT CCG GGG TAC AGT CTC GAC TGT CTT TGA
 H W E P E I P A P M S E L T E T>

-----><----- I-Ad α -TM domain -----

1400 1410 1420 1430 1440

GTG GTG TGT GCC CTG GGG TTG TCT GTG GGC CTT GTG GGC ATC GTG GTG
 CAC CAC ACA CGG GAC CCC AAC AGA CAC CCG GAA CAC CGG TAG CAC CAC
 V V C A L G L S V G L V G I V V>

1450 1460 1470 1480 1490

GGC ACC ATC TTC ATC ATT CAA GGC CTG CGA TCA GGT GGC ACC TCC AGA
 CGG TGG TAG AAG TAG TAA GTT CCG GAC GCT AGT CCA CGG TGG AGG TCT
 G T I F I I Q G L R S G G T S R>

1500

CAC CCA GGG CCT TTA TGA
 GTG GGT CCC GGA AAT ACT
 H P G P L >
 - I-Ad α -TM domain ->

-55/56

FIGURE 29 (SHEET 1 OF 4)

10 20 30 40 50

CCACC ATG GCT CTG CAG ATC CCC AGC CTC CTC CTC TCA GCT GCT GTG GTG
 GGTGG TAC CGA GAC GTC TAG GGG TCG GAG GAG GAG AGT CGA CGA CAC CAC
 M A L Q I P S L L L S A A V V>
 <----- I-Ad β chain leader ----->

60 70 80 90

GTG CTG ATG GTG CTG AGC AGC CCA AGG ACC TTA AGT ATC TCT CAG GCT
 CAC GAC TAC CAC GAC TCG TCG GGT TCC TCG AAT TCA TAG AGA GTC CCA
 V L M V L S S P R T L S I S Q A>
 ----->

100 110 120 130 140

GTT CAC GCT GCT CAC GCT GAA ATC AAC GAA GCT GGT CGT GCT AGC GGA
 CAA GTG CGA CGA GTG CGA CTT TAG TTG CTT CGA CCA GCA CGA TCG CCT
 V H A A H A E I N E A G R A S G>
 ----- OVA 323-339 -----><-----

150 160 170 180 190

GGG GGC GGA AGC GGC GGA GGG GGA AAC TCC GAA AGG CAT TTC GTG GTC
 CCC CCG CCT TCG CCG CCT CCC CCT TTG AGG CTT TCC GTC AAG CAC CAG
 G G G S G G G G N S E R H F V V>
 -- 10 amino acid linker --><----- I-Ad β -1 domain ----->

200 210 220 230 240

CAG TTC AAG GGC GAG TGC TAC TAC ACC AAC GGG AGC CAG CGC ATA CGG
 GTC AAG TTC CCG CTC ACG ATG ATG TGG TTG CCC TGC GTC GCG TAT GCC
 Q F K G E C Y Y T N G T Q R I R>
 ----->

250 260 270 280 290

CTC GTG ACC AGA TAC ATC TAC AAC CGG GAG GAG TAC GTG CGC TAC GAC
 GAG CAC TGG TCT ATG TAG ATG TTG GCC CTC CTC ATG CAC GCG ATG CTG
 L V T R Y I Y N R E E Y V R Y D>
 ----->

300 310 320 330

AGC GAC GTG CGC GAG TAC CGC CGG GTG ACC GAG CTG CGG CGG CCA GAC
 TCG CTG CAC CGC CTC ATG CGG CGC CAC TGG CTC GAC CCC CGC GGT CTC
 S D V G E Y R A V T E L G R P D>
 ----->

340 350 360 370 380

GCC GAG TAC TGG AAC AGC CAG CGG GAG ATC CTG GAG CGA AGC CGG CGC
 CGG CTC ATG ACC TTG TCG GTC CGC CTC TAG GAC CTC GCT TGC CGC CGG
 A E Y W N S Q P E I L E R T R A>
 ----->

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FIGURE 29 (SHEET 2 OF 4)

390 400 410 420 430
 * * * * *
 GAG GTG GAC ACG GCG TGC AGA CAC AAC TAC GAG GGG CCG GAG ACC AGC
 CTC CAC CTG TGC CGC ACG TCT GTG TTG ATG CTC CCC GGC CTC TGG TCG
 E V D T A C R H N Y E G P E T S>

 440 450 460 470 480
 * * * * *
 ACC TCC CTG CGG CGG CTT GAA CAG CCC AAT GTC GCC ATC TCC CTG TCC
 TGG AGG GAC GCC CCC GAA CTT GTC GGG TTA CAG CGG TAG AGG GAC AGG
 T S L R R L E Q P N V A I S L S>
 --- I-Ad β -1 domain ->----- I-Ad β -2 domain -----
 490 500 510 520 530
 * * * * *
 AGG ACA GAG GCC CTC AAC CAC CAC AAC ACT CTG GTC TGT TCG GTG ACA
 TCC TGT CTC CGG GAG TTG GTG GTG TTG TGA GAC CAG ACA ACC CAC TGT
 R T E A L N H H N T L V C S V T>

 540 550 560 570
 * * * *
 GAT TTC TAC CCA CCC AAG ATC AAA GTG CGC TGG TTC AGG AAT GGC CAG
 CTA AAG ATG GGT CGG TTC TAG TTT CAC CGG ACC AAG TCC TTA CCG GTC
 D F Y P A K I K V R W F R N G Q>

 580 590 600 610 620
 * * * * *
 GAG GAG ACA GTG GGG GTC TCA TCC ACA CAG CTT ATT AGG AAT GGG GAC
 CTC CTC TGT CAC CCC CAG AGT AGG TGT GTC GAA TAA TCC TTA CCC CTC
 E E T V G V S S T Q L I R N G D>

 630 640 650 660 670
 * * * * *
 TCG ACC TTC CAG GTC CTG GTC ATG CTG GAG ATG ACC CCT CAT CAG GGA
 ACC TCG AAG GTC CAG GAC CAG TAC GAC CTC TAC TGG GGA GTA GTC CCT
 W T F Q V L V M L E M T P H Q G>

 680 690 700 710 720
 * * * * *
 GAG GTC TAC ACC TGC CAT GTG GAG CAT CCC ACC CTG AAG AGC CCC ATC
 CTC CAG ATG TGG ACG GTA CAC CTC GTA GGG TCG GAC TTC TGG GGG TAC
 E V Y T C H V E H P S L K S P I>
 ----- I-Ad β -2 domain -----
 730 740 750 760 770
 * * * * *
 ACT GTG GAG TGG ACT ACT GGT GGC GGT GGC AGC GGC GGT GGT GGT TCC
 TGA CAC CTC ACC TGA TCA CCA CCC CCA CCG TCG CCG CCA CCA CCA AGG
 T V E W T S G G G G S G G G G G S>
 -----><----- 24 amino acid linker -----

FIGURE 29 (SHEET 3 OF 4)

780 790 800 810

GCT GGC GGC GGT TCT GGC GGT GGT TCC TCG ACT GAA GAC GAC ATT
 CCA CGG CGG CCA AGA CGG CCA CGG CCA AGG AGG TCA CTT CTG CTG TAA
 G G G G S G G G G S S S S E D D I>

820 830 840 850 860

GAG GCC GAC CAC GTA GGC TTC TAT GGT ACA ACT GTT TAT CAG TCT CCT
 CTC CGG CTG GTG CAT CGG AAG ATA CCA TGT TGA CAA ATA GTC AGA GGA
 E A D H V G F Y G T T V Y Q S P>
 ---- I-Ad α -1 domain -----

870 880 890 900 910

GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT GAT GAG TTG TTC
 CCT CTG TAA CCG GTC ATG TGT GTA CTT AAA CTA CCA CTA CTC AAC AAG
 G D I G Q Y T H E F D G D E L F>

920 930 940 950 960

TAT GTG GAC TTG GAT AAG AAG AAA ACT GTC TGG AGG CTT CCT GAG TTT
 ATA CAC CTG AAC CTA TTC TTC TTT TGA CAG ACC TCC GAA GGA CTC AAA
 Y V D L D K K T V W R L P E F>

970 980 990 1000 1010

GCG CAA TTG ATA CTC TTT GAG CCC CAA GGT GGA CTG CAA AAC ATA GCT
 CGG GTT AAG TAT GAG AAA CTC CGG GTT CCA CCT GAC GTT TTG TAT CCA
 G Q L I L F E P Q G G L Q N I A>

1020 1030 1040 1050

GCA GAA AAA CAC AAC TTG GGA ATC TTG ACT AAG AGG TCA AAT TTC ACC
 CGT CTT TTT GTG TTG AAC CCT TAG AAC TGA TTC TCC ACT TTA AAG TGG
 A E K H N L G I L T K R S N F T>
 ---- I-Ad α -1 domain -----

1060 1070 1080 1090 1100

CCA GCT ACC AAT GAG GCT CCT CAA GCG ACT GTG TTC CCC AAG TCC CCT
 CGT CGA TGG TTA CTC CGA CGA GTT CGC TGA CAC AAG GCG TTC AGG GGA
 P A T N E A P Q A T V F P K S P>

-----> I-Ad α -2 domain -----

1110 1120 1130 1140 1150

GTG CTG CTG GGT CAG CCC AAC ACC CTT ATC TGC TTT GTG GAC AAC ATC
 CAC GAC GAC CCA GTC CGG TTG TGG GAA TAG ACC AAA CAC CTG TTG TAG
 V L L G Q P N T L I C F V D N I>

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FIGURE 29 (SHEET 4 OF 4)

1160	1170	1180	1190	1200
TTC CCA CCT GTG ATC AAC ATC ACA TGG CTC AGA AAT AGC AAG TCA GTC AAG GGT GGA CAC TAG TTG TAG TGT ACC GAG TCT TTA TCG TTC AGT CAG F P P V I N I T W L R N S K S V>				
<hr/>				
1210	1220	1230	1240	1250
ACA GAC GGC GTT TAT GAG ACC AGC TTC CTC GTC AAC CGT GAC CAT TCC TGT CTG CCG CAA ATA CTC TGG TCG AAG GAG CAG TTG GCA CTG GTA AGG T D G V Y E T S F L V N R D H S>				
<hr/>				
1260	1270	1280	1290	
TTC CAC AAG CTG TCT TAT CTC ACC TTC ATC CCT TCT GAT GAT GAC ATT AAG GTG TTC GAC AGA ATA GAG TGG AAG TAG GGA AGA CTA CTA CTG TAA F H K L S Y L T F I P S D D D I>				
<hr/>				
1300	1310	1320	1330	1340
TAT GAC TGC AAG GTG GAG CAC TGG GGC CTG GAG GAG CCG GTT CTG AAA ATA CTG ACG TTC CAC CTC GTG ACC CCG GAC CTC CTC GGC CAA GAC TTT Y D C K V E H W G L E E P V L K>				
<hr/> ----- I-Ad a-2 domain -----				
1350	1360	1370	1380	
CAC TGG GAG GAA GAA GAG TAC CCG ATG GAA TGA GTG ACC CTC CTT CTT CTC ATG TAC GGC TAC CTT ACT H W E E E E Y M P M E *>				
<hr/> ----- EE tag ----->				